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January 13, 2005, 01:14:40; Search time 77.2131 Seconds (without alignments) 46.460 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 TRLTRKDGLK 10
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geneseqp1980s:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aav30691 Apo-B100			7 Apo B	Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b	80		1 Hume	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo	_	Adj57400 Human apo	7 Human	2	Aaw96826 Amino aci	Aau98981 Human apo	Add48677 Human Pro	Aao15893 Human apo	Ahr40253 Human ali
SUMMARIES DB ID	2 AAY30691	-		2 AAW57207	2 AAW41261	2 AAW96892	6 ABJ37575	2 AAW57208	2 AAW57209	5 AAE14541	2 AAW96876	2 AAW64587	2 AAW96845	4 ABB37687	4 ABG52504	2 AAR72704	2 AAR34031	8 ADJ57400	2 AAY31237	2 AAW41262	2 AAW96826	5 AAU98981	7 ADD48677	5 AAO15893	6 ABR40253
Length D	10	10	11	13	15	15	20	22	22	34	36	37	51	343	343	377	377	2463	3923	4536	4536	4560	4561	9	4563
% Query Match	100.0	92.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0		84.0
Score	50	46	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
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	Add44981 Rat Prote Add44987 Human Proc Add44987 Human Pro Add68663 Human hea Add18720 Human sof Aae27989 Human enz Adj68303 Human enz Adj68303 Human hea
ABU79140 ADF43408 ADH18871 ADH18870 ADH33445 ADG33447 AAU33184 AAX30700 AAX30682 AAX30687	ADD44981 ADD44985 ADD44983 ADD48663 ADQ18720 ARZ7989 ADJ68303 ADG8303
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6 4 4 4 4 4 4 4	
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ALIGNMENTS

RESULT 1

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. AAY30691 standard; peptide; 10 AA Claim 17; Page 57; 70pp; English. 98US-0077618P. 99WO-US004805. Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999. AAY30691; AAY30693

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acide 335t to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

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Gaps

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DB 2; Length 10; 0; Indela

Score 46; DB 2; Pred. No. 0.02; 1; Mismatches

92.0%;

Query Match Best Local Similarity

Sequence 10 AA;

9; Conservative

Matches

1 TRLTRKDGLK 10 |||||||||||| TRLTRKEGLK 10

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3158 to 3167 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (EQ). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assy methods for identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the connection atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                              Gaps
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                                                                                   100.0%; Score 50; DB 2; Length 10; 100.0%; Pred. No. 0.003; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       AAY30690 standard; peptide; 10 AA.
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                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                   Local Similarity
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                                                                                                                                Sequence 10 AA;
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Matches
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Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.

Apo B binding site peptide 2.

(first entry)

03-AUG-1998

AAW57205;

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Baillie

Halbert GW, Owens MD,

(UYST) UNIV STRATHCLYDE.

97WO-GB002610,

25-SEP-1997;

27-SEP-1996;

WO9813385-A2

Synthetic.

02-APR-1998

AAW57205 standard; peptide; 11 AA.

AAW57205 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a specifically claimed Apo B binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKNKHRH (1) or TRILITKRGIK (2), or their dimers Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells drug-targeting vectors for delivering anticancer drugs to cancer cells culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 52; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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Best Local Similarity
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Synthetic

AAW57207;

RESULT 4

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This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apob-100). IL-KAQ-XI-KKKMKHR15-X2-T-Z2 (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids ac Compositions containing the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-as peptide, inhibits active as such or as part of a 98-as peptide, inhibits activation of the prothrombinase complex; and prevents activation of the gradue of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (1) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                         Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 42; DB 2; Length 15; 90.0%; Pred. No. 0.2; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 22; 60pp; English.
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                                                               Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                97WO-GB001255.
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                   (first entry)
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TRLTRKRGLK
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                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                   WO9743311-A1
                   19-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their cimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                  Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "attached to retinoic acid"
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Pred. No. 0.17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baillie G;
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                                                             AAW57207 standard; peptide; 13 AA.
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90.0%;
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Modified-site
                                                                                                                                                          03-AUG-1998
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Gaps

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Query Match

Matches

AAW41261

RESULT 5 AAW41261

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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acide. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                        one sulfated or sulfonated amino rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 6; Length 20;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                   Щ.
                                                                                                                                                                    Use of a ligand comprising of at least acid for the treatment of e.g. tumors,
                                                                                                   Maynard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                             Disclosure; Fig 2; 79pp; English.
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           20-JUL-2001; 2001US-0306726P
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                                                                                                   Schoenmakers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                          retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLIRKDGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TRLTRKRGLK 16
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                                                                                                                                    WPI; 2003-300420/29.
                                            ETH ZUERICH
UNIV ZURICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998
                                                                                               Hubbell JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                            (ETHZ-)
                                                               (DXZO-)
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apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological; cardiovascular, circulatory, ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in viro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96878-97 represent nuclear localisation signal sequence derived from
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Mismatches
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                                                                                                                                                                                                                                                                                                                 Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin binding peptide sequence #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE
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                                                                                                                                                                                                                   97US-00874807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-2002; 2002WO-US023419.
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                         Homo sapiens
                                                                                                                                                                                                                   13-JUN-1997;
14-MAY-1998;
                                                                                                                                                                                 10-JUN-1998;
                                                                                                          WO9856938-A1
                                                                                                                                              17-DEC-1998.
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                                                                                                                                                                                                                                                                                                             Guevara JG,
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                                                                                                                                                                                                                                                                                                                                                                                                                      treatment.
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RESULT 7

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Gaps

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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-maturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKKHKHR (1) or TTRLTRKRGIK (2), or their cimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
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Pred. No. 0.29;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "attached to retinoic acid"
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              Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                84.0%;
90.0%;
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                    Sequence 22 AA;
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

peptide binding to apo B protein delivering drugs to cancer cells

Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.

Claim 13; Fig 7; 73pp; English.

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Gaps

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          peptide component that has at least 1 binding site for an ago B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an ago B binding sequence with at least 10% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRKIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) frung-targeting vectors for delivering anticancer drugs to cancer cells that express an ago B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete ago B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL, in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-impulsinedpendent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidised low density lipoprotein, oxLDL, immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
particle of the present invention. The LDL particle comprises at least 1
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                                                                                                                                                                                                                                                                                                               84.0%; Score 42; DB 2; Length 22; 90.0%; Pred. No. 0.29; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE14541 standard; peptide; 34 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ARKT-) ARK THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                        Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide p62.
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Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The present specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in wiro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                               Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                              Score 42; DB 5; Length 34;
Pred. No. 0.47;
Mismatches 1; Indels
                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2; Length 36;
Pred. No. 0.5;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                       AAW96876 standard; peptide; 36 AA.
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                                                                              84.0%;
90.0%;
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98US-00079030.
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                       9; Conservative
                                                                                                                                    1 TRLTRKDGLK 10
                                                                                                                                                                  34
                                                                                                                                                         25 TRLTRKRGLK
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070331/06.
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Best Local Similarity
Matches 9; Conserv
                                           Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                    22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998,
                                                                                                                                                                                                                                                                     AAW96876;
                                                                                           Best Loc
Matches
                                                                                                                                                                                                            RESULT 11
AAW96876
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Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.

Example 2; Page 9; 18pp; German,

Schenk V;

Lang H,

Moritz B, Kiessig S,

(IMMO) IMMUNO AG.

WPI; 1998-416142/36.

98EP-00890007, 97AT-00000044

12-JAN-1998; 13-JAN-1997;

Factor V, human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.

Homo sapiens

EP857973-A2 12-AUG-1998.

Human apolipoprotein peptide fragment #1.

(first entry)

23-OCT-1998

AAW64587;

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AAW64587 standard; peptide; 37 AA.

RESULT 12

AAW64587

11 TRLTRKRGLK 20

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AWM64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions). Particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of developing of apos indicates increased risk of developing Alzheimer's calleles of apos indicates increased risk of developing Alzheimer's disease), thermostable 5.10-methylenetetrahydrofolate reductase correct associated with increased risk of cardiovascular disease). The mutations (associated with increased risk of cardiovascular disease). The prions. The method does not require complex apparatus for polymerase correct chain reactions, it is simple, standardisable and reliable and is paramile to he mannifications or analogous and regularly suited to routine screening. It also allows mutant protein in a sammle to he mannifications.
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Pred. No. 0.51;
0; Mismatches 1; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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90.0%;
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Best Local Similarity
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Matches
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ID AAW9
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Gaps

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84.0%;

9; Conservative

TRLTRKDGLK 10

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR
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                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                        21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                 2000US-0207456P
                                                                                                  30-JAN-2001; 2001WO-US000669
                                                                                                                                                      2000US-0180312P
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2000US-0207456P
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nes 9; Conserv
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WO200157277-A2
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2003
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                                                                                                                                                                         Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arcerlosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 42; DB 2; Length 51; 90.0%; Pred. No. 0.72;
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                                                                                                                        Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 151; 293pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00874807.
98US-00079030.
                                                                    22-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1998;
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                     AAW96845;
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ઠે 셤

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Gaps

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Indels

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Chen W, Rank DR;
  (MOLE-) MOLECULAR DYNAMICS INC.
       Hanzel DK,
             WPI; 2001-488898/53
        Penn SC,
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences Claim 27; SEQ ID NO 31152; 658pp; English.

Sequence 343 AA;

Gaps ; 0 84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.5; live 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9; Conservative

1 TRLTRKDGLK 10 ò

|||||| ||| 169 TRLTRKRGLK 178

Search completed: January 13, 2005, 01:43:00 Job time : 79.3798 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein January 13, 2005, 01:30:05 ; Search time 14.4262 Seconds (without alignments) 66.696 Million cell updates/sec Run on:

US-09-823-418-10 50 1 TRLTRKDGLK 10 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	42	84.0	965	2	S32802	apolipoprotein B -
7	42	84.0	4563	-	LPHUB	apolipoprotein B-1
e	38	76.0	269	7	C60950	apolipoprotein B-1
4	38	76.0	389	Н	DEPGPA	pyruvate dehydroge
S	38	76.0	390	Н	DEHUPA	
9	38	76.0	390	Н	DERTP1	pyruvate dehydroge
7	38	76.0	390	7	DERTPA	
80	38	76.0	390	7	S23506	pyruvate dehydroge
6	38	76.0	779	7	JH0102	
10	36	72.0	275	7	E60950	apolipoprotein B-1
11	36	72.0	394	7	T46858	molybdenum cofacto
12	35	70.0	227	~	A84109	ABC transporter (A
13	35	70.0	325	7	T29604	hypothetical prote
14	35	70.0	480	7	G71050	asparagine synthas
15	34	68.0	131	7	A11540	hypothetical prote
16	34	68.0	190	7	G82634	hypothetical prote
17	34	68.0	857	7	T37459	ರ
18	33	0.99	453	~	G83043	probable transport
19	33	0.99		~	C82421	conserved hypothet
20	33	0.99			S34191	sulfite reductase
21	33	v		Н	S74619	hypothetical prote
22	33	0.99	772	~	I50463	protein kinase - c
23	32	64.0	206	~	B97282	ribosomal protein
24	32	64.0	208	7	C82742	transcription regu
25	32	4.	266	7	C72380	hypothetical prote
26	32	64.0	272	~	E83363	
27	32	64.0	274	N	A60950	•⊣
28	32	64.0	280	~	806572	finger protein (cl
59	32	64.0	289	~	A70751	hypothetical prote

pyruvate dehydroge	pyruvate dehydroge	probable major tai	probable bacteriop	hypothetical prote	glycerol-3-phospha	hypothetical prote	hypothetical prote	transcription anti	transcription anti	apolipoprotein B-1	translation elonga	hypothetical prote	probable pol polyp	ribosomal protein	hypothetical prote
A49360	DEHUPT	AG0929	AI0836	H72393	C45868	D81265	S69723	AC1408	AC1784	JH0101	S43748	T32289	T18348	S51055	T28840
~	Н	~	7	7	7	7	7	~	7	~	7	~	~	~	7
370	388	390	390	473	555	584	687	689	689	784	819	833	1199	26	151
64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	62.0	62.0
	2	32	32	32	32	32	32	32	32	32	32	32	32	31	31
32	**1														

ALIGNMENTS

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apolipoprotein B - crab-eating macaque (fragment)

G.Species: Macaca fascicularis (crab-eating macaque)

G.Species: Macaca fascicularis (crab-eating macaque)

G.Species: Oc-Jan-1995 #sequence_revision O6-Jan-1995 #text_change O9-Jul-2004

G.Accession: 832802

B.Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchi Biochim. Biophys. Acta 1086, 325-334, 1991

A.Reference number: 832802; MUD: 92075708; PMID: 1742325

A.Reference number: MUD: 92075708; PMID: 1742325

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Molecule type: mRNA

A.Residues: 1-596 cApp>

A.Kossa-references: UNIPROT: Q28473; EMBL: X15737; NID: 938047; PIDN: CAA33755.1; PID: 99301

C; Superfamily: apolipoprotein B
RESULT 1
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Gaps . 0 Length 596; 1; Indels Score 42; DB 2; Pred. No. 2.1; 0; Mismatches 84.0%; 90.0%; Query Match
Best Local Similarity 90.0
Matches 9; Conservative

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226 TRLTRKRGLK 235 1 TRLTRKDGLK 10 g ò

- human apolipoprotein B-100 precursor

Applitoprocein B-10 precursor - numan NyContains apolipoprotein B-26; apolipoprotein B-74 c; Species: Homo sapiens (man) S, Sz263; AZ5263; AZ5263; AZ4684; AZ3817; AZ3817; AZ3817; AZ3817; BZ7859; BBCkhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; SC A; Tildwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; SC A; Tilde: DNA sequence of the human apolipoprotein B gene.

A; Reference number: AZ7850
A; Accession: AZ2850
A; Accession: AZ2850
A; Residues: 1-617, A', 619-1929, F', 1931-3318, D', 3320-3426, T', 3428-3431, Q', 3433-3731, A; Residues: U-617, A', 619-1929, F', 1931-3318, D', 3320-3426, T', 3428-3431, Q', 3433-3731, A; Cross-references: UNIPROT:P04114; UNIPROT:P3482; UNIPROT:P3492; UNIPROT:Q9UMNO; UNI B; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I. EMBO J. 5, 3495-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: r A; Reference number: A3058; MUID:87161758; PMID:3030729
A; Molecule type: mRNA
A; Residues: 1-11.15-2339, S', 2541-3823, F', 3825-4563 < CLA>
A; Note: 1109-Asp was also found
R; Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

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Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E. Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than or A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Reference number: A29287
A;Molecule type: mRNA
A;Residues: 3846-4298 «SHO>
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A;Title: Isolation, expression and characterization of a human apolipoprotein B 100-special and characterization of a human apolipoprotein B 100-special and a control and characterization of a human apolipoprotein B 100-special and a control and characterization of a human apolipoprotein B 100-special and a control and a cont
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Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985

A; Reference number: A24738

A; Accession: A24738

A; Accession: A24738

A; Molecule type: mRNA

A; Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',3:
A; Cross-references: GB:M12413; NID:g178735; PIDN:AA551742.1; PID:g178736

B; Chen, S.H.; Habib, G; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Ca' A; Tille: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in A; Reference number: A40133; MUID:88018019; PMID:3659919
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A. Molecule type: Molida
A. Molida
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Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990 A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human at A; Reference number: A55783; MUID:90319144; PMID:2115173
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A, Residues: 2129-2179, 2181-2235 < HA2>
A, Residues: 2129-2179, 2181-2235 < HA2>
A, Residues: 2129-2179, 2181-2235 < HA2>
A, Round and B, Molectine B, Mol
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A; Residues: 3056-3159 <MEH>
A; Cross-references: GB: X03045; NID: g28783; PIDN: CAA26850.1; PID: g929609
A; Cross-references: GB: X03045; NID: g28783; PIDN: CAA26850.1; PID: g929609
R; Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in human intestine
A; Reference number: A29659; MUID: 88049670; PMID: 2445342
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A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-
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A;Residues: 4219-4337,'S',4339-4563 <PFI>A;Cross-references: GB:M36676
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A; Residues: 2169-2179 < HOS>
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A;Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A;Reference number: A93639; MUID:87016385; PMID:3763409
A;Accession: A25263
A;Accession: A25263
A;Molecule type: mRNA
A;Residues: 1-272,'N',274-617,'A',619-1217,'E',1219-2091,'V',2083-2364,'T',2366-2679,'Q'
A;Cross-references: GB:X04506; NID:934330; PIDN:CAA28191.1; PID:934331
B;Law, S.W.; Grant, S.W.; Higopatchia, K.; Lee, N.; Brewer JT
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A;Title: Human liver apolipoprotein B-100 CDNA: complete nucleic acid and derived amino
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A; Molecule type: mRNA
A; Residues: 1-97, II, 99-328, VV, 330-644, II, 646-918, PV, 920-3318, DV, 3320-3426, TV, 3428-44.82 (C. 4134-4180, EV, 4182-4563 (CHE)
A; Cross-references: GB: J02610; NID: G178803; PIDN: AA35549.1; PID: G178804
A; Notes: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides R; Notter: A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; Hroc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein A; Reference number: A24320; MUID: 86287319; PMID: 3461454
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A; Residues: 485-617, A', 619-1044 <LA2>
A; Residues: 485-617, A', 619-1044 <LA2>
A; Residues: 485-617, A', 619-1044 <LA2>
A; Crotter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proct. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a CDNA clone encoding the amino-terminal region of human apolipopy
A; Reference number: A94088; MUID:86149325; PMID:3513177
A; Molecule type: mRNA
A; Residues: 1-291 <PRO>
A; Cross-references: GB:MI2681; NID:g178797; PIDN:AA51753.1; PID:g178798
A; Cross-references: GB:MI2681; NID:g178797; PIDN:AA51753.1; PID:g178798
B; Crotter Natl. Acad. Sci. U.S. A. 82, 4986, 1985
A; Title: A partial CDNA clone for human apoliprotein B.
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A.Molecule type: mRNA
A.Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
A.Molecule type: mRNA
A.Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
A.Mote: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
A.Mote: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
A.Mote: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
A.Mote: The complete codons given for residues and maino acid sequence of human apolipoprotein B-100.
A.Reference number: A92556; MUID:87008488; PMID:3759943
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A,Residues: 1-97, I', 99-617, 'A',619-941, 'XXIMSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSPOE
A,Residues: 1-97, I', 99-617, 'A', 619-941, 'XXIMSLPPKP', 951-1138,'PTGRLPNCFSNGLICYSLWLHSPOE
B,R. Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, U; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
A;Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A;Reference number: A24684; MUID:86094221; PMID:3001697
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A; Reaidues: 1282-2721, 2742-3290, 'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A; Cross-references: GB.M15421; NID:9178817; PIDN:AA51758.1; PID:9178818
R; Hardman, D.A.; Protter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
Biochemistry 26, 5478-5486, 1987
A; Title: Structural comparison of human apolipoproteins B-48 and B-100.
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A; Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 <DEE>
A; Cross-references: GB: K03175; NID: G178821; PIDN: AAA51759.1; PID: G178822
R; Carleson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
Gene 49, 29-51, 1986
A; Title: Analysis of the human apolipoprotein B gene; complete structure of the
A; Reference number: A91565; MUID: 87191999; PMID: 2883086
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A;Residues: 1671-2323,'PYW',2327-2352,'H',2354-2398 <HAR>
A;Cross-references: GB:M17367; NID:g178731; PIDN:AAA51741.1; PID:g178732
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A; Residues: 3113, 'L',3115-3130,'R',3132-3133,'P',3135-3136,'R' <LE2>
B; Beackhart's B.D: idudwig, E.M.; Perotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.; J. Biod. Chem. 261, 15364-15367, 1986
A; Title: Structure of the human apolipoprotein B gene.
A; Reference number: A9264; MID: 87057133; PMID: 2946672
A; Contents: annotation; gene structure
B; Wagener, R.; Pfitzner, R.; Stoffel, W.
Biol. Chem. 4Depe-Seyler 368, 419-425, 1987
A; Title: Studies on the organization of the human apolipoprotein B 100 gene.
A; Reference number: A90715; MUID: 87271140; PMID: 2866136
A; Contents: annotation; gene structure
B; Weisgraber, R.H.; Rall Jr., S.C.
J; Biol. Chem. 262, 11097-11103, 1987
A; Title: Human apolipoprotein B: 1000 heparin-binding sites.
A; Reference number: A92605; MUID: 87280197; PMID: 3301850
A; Contents: annotation; heparin binding and disulfide bond
B; Dashti, N.; Lee, D.M.; Mok, T.
Biochem: Biophys. Res. Commun. 137, 493-499, 1986
A; Title: Apolipoprotein B is a calcium binding protein.
A; Reference number: A9015; MUID: 8624245; PMID: 3087360
A; Contents: annotation; calcium binding protein.
A; Title: Apolipoprotein B is a calcium binding protein.
A; Title: Apolipoprotein B; WuiD: 8624245; PMID: 3087360
A; Contents: annotation; calcium binding protein.
A; Title: Molecular cloning of human apolipoprotein B CDNA.
A; Reference number: 137178; MUID: 86093680; PMID: 3841204
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C60950
R;Law, A.; Scott, J.
J. 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A;Reference number: A60950; MUID:90324804; PMID:2373961
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A;Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. PEBS Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
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Pred. No. 15;
0; Mismatches 1; Indels
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Pred. No. 6.2;
1; Mismatches
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                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 873-892,'K',894-896 <LE1>
A;Accession: B22006
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90.0%;
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216 SRLTRKRGLK 225
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Best Local Similarity
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Matches 8; Conserv
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RESULT 4

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Dyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain precursor - pig (fragment)

NiAlternate names: pyruvate dehydrogenase complex, El component alpha chain

C; Species Sus scrofa domestica (domestic pig)

C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C; Accession: S20813

R; Sermon, K; DeMeirleir, L; Elpers, I; Lissens, W; Liebaers, I.

R; Sermon, K; DeMeirleir, L; Elpers, I; Lissens, W; Liebaers, I.

R; Reference number: S20813

A; Reference number: S20813

A; Residues: 1-389 <SER>
C; Superimental source: muscle
C; Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bic; Kerywords: flavoprotein; heterochendrion; (fragment) #status predicted <TNP>
F; 29-28 / Domain: transit peptide (mitochondrion) (fragment) #status predicted <TNP>
F; 29-28 / Domain: thiamin pyrophosphate-binding domain homology <TPB>
F; 29-28 / Domain: thiamin pyrophosphate (Ser) (covalent) #status experimental
F; 292 / Binding site: phosphate (Ser) (covalent) #status experimental
F; 299 / Binding site: phosphate (Ser) (covalent) #status experimental
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A,Residues: 1-390 <40L.
A,Cross-references: GB:M24848; NID:g190761; PIDN:AAA36533.1; PID:g190762
A,Cross-references: GB:M24849; N.; Wah, A.M.L.H.; Robinson, B.H.
R;De Meirleir, L.; MacKay, N.; Wah, A.M.L.H.; Robinson, B.H.
A;De Meirleir, Chm. 263, 1991-11995; 1988
A;Title: Isolation of a full-length complementary DNA coding for human E-1-alpha subunn
A;Reference number: A28275; MUID:88115327; PMID:2828359
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A;Residues: 1-344, Pr., 350-353,'A',355-390 <DEM1>
A;Cross-references: EMBL:103503; NID:9189765
A;Note: the translated sequence in GenBank entry HUMPDHE1B, release 114.0, (PIDN:AAA600
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R;Ho, L.; Wexler, I.D.; Liu, T.C.; Thekkumkara, T.J.; Patel, M.S.
Proc. Natl. Acad. Sci. U.S.A. 86, 5330-5334, 1989
A;Title: Characterization of CDNAs encoding human pyruvate dehydrogenase alpha-subunit.
A;Reference number: A33905; MUID:89315791; PMID:2748588
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submitted to the EMBL Data Library, April 1990
A;Description: Identical sequences for human brain and liver pyruvate dehydrogenase El
A;Reference number: S11715
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53 TVLTREDGLK 62
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Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-390 <HU1>
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A;Readdues: 1-390 «CULD»

A;Readdues: 1-390 «CULD»

A;Cross-references: EMBL: 212158; NID:957656; PIDN: CAA78146.1; PID:957657

A;Cross-references: EMBL: 212158; NID:957656; PIDN: CAA78146.1; PID:957657

A;Note: in Genbank entry RRPDHYELA, release 113.0, the source is designated as Rattus r;
C;Superfamily: pyruvate dehydrogensee (lipoamide) alpha chain; thiamin pyrophosphate-bil
C;Keywords: flavoprotein; heterotetramer; mitochondrion; oxidoreductase; phosphoprotein
F;1-29/Domain: transit peptide (mitochondrion) #status predicted <nNP>
F;185-230/Product: pyruvate dehydrogensee (lipoamide) alpha chain #status predicted <NAT
F;293/Anding site: phosphate (Ser) (covalent) #status predicted
F;293/Anding site: phosphate (Ser) (covalent) #status predicted
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A,Residues: 1.390 <MAT1>
A,Cross-references: UNIPROT:P26284
A,Cross-references: UNIPROT:P26284
C,Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bli C,Keywords: flavoprotein, heterotetramer; mitochondrion; oxidoreductase; phosphoprotein, F;1-29/Domain: transit peptide (mitochondrion) #status predicted <MTP>
F;1-29/Domain: transit peptide (mitochondrion) #status predicted <MTP>
F;30-390/Product: pyruvate dehydrogenase (lipoamide) alpha chain #status predicted <MAT:
F;185-234/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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A; Residues: 1-390 <CULS>
A; Residues: 1-390 <CULS>
A; Cross-references: Universitive
A; Experimental source: liver
B; Cullingford, T.E.; Clark, J.B.; Phillips, I.R.
J. Neurochem. 62, 1682-1690, 1994
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C;Species: 31-Dec.1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: S21553; 156503
R;Cullingford, T.E.; Phillips, I.I.; Clark, J.J.
submitted to the EMBL Data Library, June 1992
A;Reference number: S21553
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80.0%; Pred. No. 8.9;
tive 1; Mismatches 1; Indels
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A,Accession: 156503
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                            1;
                            Score 38; DB 1;
Pred. No. 8.9;
                                                                                                                                            1; Mismatches
                            76.0%;
                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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54 TVLTREDGLK
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54 TVLTREDGLK
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A; May position: Xp22.1.Xp22.1.
A; May position: Xp22.1.Xp22.1.
A; Introns: 19/3; 23/3; 97/3; 140/1; 170/3; 201/3; 253/3; 272/3; 300/2; 336/3
C; Complex: the El component (pyruvate dehydrogenase) is a heterotetramer of two alpha any yltransferase) monomers and 6 E3 component (lipoamide dehydrogenase) dimers
C; Punction:
C; Punction:
C; Punction: catalyzes the reaction of pyruvate and lipoamide (on the E2 component) to 6 pyruvate by NAD to form acetyl-CoA, carbon dioxide and NADH
A; Pathway: pyruvate metabolism
A; Pathway: pyruvate metabolism
A; Note: thiamin pyrophosphate [lipoamide) alpha chain; thiamin pyrophosphate-bin C; Keywords: flavoprotein; heterotetramer; mitochondrion; oxidoreductase; phosphoprotein; F; 1-29/Domain: transit peptide (mitochondrion) alpha chain #status predicted chydrogenase (lipoamide) alpha chain #status predicted chydro
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 374-382, 'SVDQV' <170
A;Cross-references: GB:S56181; NID:g299257; PIDN:AAB25674.1; PID:g299258
R;De Meirleir, L.; Lissens, W.; Vamos, E.; Liebaers, I.
Hum. Genet. 88, 649-652, 1992
A;Title: Pyruvate dehydrogenase (PDH) deficiency caused by a 21-base pair insertion muta
A;Reference number: I54262; MUID:92201830; PMID:1551669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 300-307, PPHSYRTREEL: 308-311 <HAN>
A;Cross-references: GB:S75842; NID:g861533; PIDN:AAB32351.1; PID:g861534
C;Comment: The phosphorylation of several serine sites by [pyruvate dehydrogenase (lipoamplex. The enzyme is dephosphorylated by [pyruvate dehydrogenase (lipoamplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule Fype: MRNA
A, Residues: 300-305, 'DSYRTRE', 306-309 < DEM2>
A, Cross-references: GB:S89908; NID:9247722; PIDN:AAB21863.1; PID:9247723
R; Hansen, L.L.; Horn, N.; Dahl, H.H.; Kruse, T.A.
Hum. Mol. Genet. 3, 1021-1022, 1994
A; Title: Pyruvate dehydrogenase deficiency caused by a 33 base pair duplication in the A; Reference number: 154356; MUID:95038723; PMID:7545958
A; Cross-references: EMBL:X52709; NID:935378; PIDN:CAA36933.1; PID:935379
                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-390 <HU2>
A;Cross-references: EMBL:X52710; NID:935380; PIDN:CAA36934.1; PID:935381
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                             A; Experimental source: brain
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apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Datesion: B60950
R;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LE A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-275 <LAW>
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoproteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molybdenum cofactor biosynthesis protein A [imported] - Rhodobacter sphaeroides C; Species: Rhodobacter sphaeroides C; Species: Rhodobacter sphaeroides C; Species: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 12-Jul-2004 C; Adcession: T4688 B; Rylackenzie, C.; Simmons, A.E.; Kaplan, S. A; Title: Multiple chromosomes in bacteria. The Yin and Yang of trp gene localization in A; Reference number: Z24108; MulD:99442363; PMID:10511537 A; Residue: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-394 <MAC>
A; Residues: 1-305  A; Residues: 1-305 A; Residues: 1-305 A; Residues: 1-305 A; Residues: 1-305 A
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C;Species: Bacillus halodurans
C;Species: Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: AB4109
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Ree. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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C;Superfamily: molybdenum cofactor biosynthesis protein, MoeA type
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87.5%; Pred. No. 23;
iive 1; Mismatches
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Pred. No. 16;
0; Mismatches
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80.0%;
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Best Local Similarity 87.5.
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642 SRLTRKRGLK 651
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                                           TRLTRKDGLK
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Best Local Similarity
Matches 8; Conserv
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A84109
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R;Fitzgerald, J.; Hutchison, W.M.; Dahl, H.H.M.
Biochim. Biophys. Acta 1131, 83-90, 1992
A;Title: Isolation and characterisation of the mouse pyruvate dehydrogenase Elalpha gene A;Reference number: S23506; MUID:92256495; PMID:1581363
A;Accession: S23506
A;Status: preliminary
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A;Note: this is a revision to the sequence from reference JH0101
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 3.09-310, 1390
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap A;Reference number: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-390 <FIT>
A,Cross-references: UNIPROT:P35486; EMBL:M76727; NID:9200276; PIDN:AAA53046.1; PID:92002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: pdha-1
C,Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bir
C,Keywords: mitochondrion; oxidoreductase; phosphoprotein
F;185-234/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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C;Superfamily: apolipoprotein B
C;Kywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein B - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
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F;232/Binding site: phosphate (Ser) (covalent) #status predicted F;293/Binding site: phosphate (Ser) (covalent) #status predicted F;300/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                       Score 38; DB 1; Length 390;
Pred. No. 8.9;
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Pred. No. 8.9;
1; Mismatches 1; Indels
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80.0%;
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Similarity 80.0%;
8; Conservative 1
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submitted to GenBank, June 1990
A;Reference number: A3864
A;Accession: JH0102
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54 TVLTREDGLK 63
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54 TVLTREDGLK 63
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A;Residues: 1-779 <SMI>
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A;Status: preliminary

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Search completed: January 13, 2005, 01:52:36
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329 TKLAREDGVK 338
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74 TRIQRKDGV 82
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A;Molecule type: DNA
A;Residues: 1-131 <GLA>
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A;Molecule type: DNA
A;Residues: 1-227 <STO>
A;Residues: 1-227 <STO>
A;Cross-references: UNIPROT:09K6Q5; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB073
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3673
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
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A;Cross-references: UNIPROT:O58829; GB:AP000005; NID:g3236132; PIDN:BAA30201.1; PID:d103
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - Pyrococcus hori)
C;Species: Pyrococcus horikoshii
Diate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: G71050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphanted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid ZK816.
A; Reference number: Z20649
A; Reference number: Z20649
A; Accession: T29604
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-325
A; Residues: 1-325
A; Cross-references: UNIPROT: Q23612; EMBL: U41018; PIDN: AAAB2327.1; CESP: ZK816.5
A; Genetics: Z4/1; 111/3; 170/2; 228/3; 280/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ZK816.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25604
R;Nhan, M:; Le, T.
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148 TRIMRKNGMK 157
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Best Local Similarity
Matches 7; Conserv
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hypothetical protein lin0865 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Al1540
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
I, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M
A;Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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Pred. No. 20;
2; Mismatches
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Best Local Similarity 66.7°,
6; Conservative
1 TRLTRKDGLK 10
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TISSUE-Liver;
MEDLINE=92075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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NCBI_TaxID=9541;
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SEQUENCE 41
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Ogywi2 oryzias lat
013788 homo sapien
P04114 homo sapien
072600 homo sapien
0911x8 bos taurus
P09804 sus scrofa
P08559 homo sapien
P35486 mus musculu
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QBbxw9 macaca fasc

Aah07142 mus muscu

Q66g29 brachydanio

Q7710 diceros bic

Q7y10 diceros bic

Q7y704 rousettus a

Q7y704 rousettus a

Q7y108 chaetophrac

Q7104 agouti paca

Q71171 hydrochoeru

Q71171 hydrochoeru

Q71172 erethizon d

Q60536 mesocricetu

Q60537 mesocricetu
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                                                                                                    January 13, 2005, 01:15:45; Search time 78.0328 Seconds (without alignments) 73.735 Million cell updates/sec
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090vv5
P79997
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Q96rk2
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                               1825181 segs, 575374646 residues
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ODPA_PIG
ODPA_HUMAN
ODPA_MOUSE
ODPA_RAT
Q8HXW9
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Maximum Match 100%
Listing first 45 summaries
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Q9PW12
Q13788
APB HUMAN
Q7Z600
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Q6DGZ9
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Q90VV5
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Q7YR10
Q7YQM8
Q7YQM7
Q7YR04
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Q60537
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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1 TRLTRKDGLK 10
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Maximum DB 8
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095211 homo sapien
Cag33416 homo sapien
Cag33416 xanthomonas
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Q8p9v7 xanthomonas
Q71z77 gallus gall
Q7ygn2 phalanger o
Q9zfa5 rhodobacter
Q7ygm9 ornithorhyn
Q7ygn0 tachyglossu
Q7tn70 dinomys bra
Q73173 treponema d
Aas12506 treponema
Q8aaw5 bacteroides
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548396; AAP97352.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini; Cercopithecidae;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 5.8;
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                095211
SECU HUMAN
CAG33416
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Q9E277
Q7E277
Q7EQX
Q7EQX
Q7EQX
Q7EQX
Q7TU70
Q73L73
AAS12506
Q8AAWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actus vociferans (Spix's owl monkey).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apolipoprotein B 100 (Fragment).
Name=apoB-100;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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SEQUENCE FROM N.A. MEDLINE-902.1771; PubMed=9578459; MEDLINE-902.1771; PubMed=9578459; Mikami T., Kusakabe T., Suzuki N.; "Molecular cloning of cDNAs and expression of mRNAs encoding alpha and "Molecular cloning of cDNAs and expression of mRNAs encoding alpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
      Soluble guanylyl cyclase alpha subunit (BC 4.6.1.2).
Oryzias latipse (Medaka fish) (Japanese ricefish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Bacanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryzinae, Atherinomorpha,
                                                                                                                                                                                                                                                beta subunits of soluble guanylyl cyclase from medaka fish Oryzias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Metaleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2; Length 678;
Pred. No. 9.9;
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88.9%; Pred. No. 9.9;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISGUE-Brain;
Shiga T., Suzuki N.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB115703; BAC80220.1; -.
EMBL; AB115703; BRC80220.1; -.
GO; GO:01004383; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:007242; P:intracellular signaling cascade; IEA.
InterPro; IPR001054; Gcyclase.
PF00211; Guanylate_cyc; 1.
SM0044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                         GO, GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:007242; F:intracellular signaling cascade; IEA.
InterPro; IPR001054; G_cyclase.
Ffam; PF00211; Guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 AA; 75133 MW; 3A6141D2A6475D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75128 MW; C03C174B535ACCD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00452; GUANYLATE CYCLASES 1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble guanylyl cyclase alphal subunit.
Name-OcGCS-alphal;
Oryzias curvinotus (Hynann ricefish).
                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 253:42-48(1998).
EMBL; AB000849; BAA19198.1; -.
HSSP; P30803; 1AZS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=104658;
                                                                                                                                                                                                                                                                   latipes.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
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"Apo B metabolism in the cynomolgus monkey: evidence for post-
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88.9%; Pred. No. 9.9;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      Length 596;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                     Murray R.,
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morinaga C., Yamamoto T., Moriya Y., Suzuki N.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062171; BAB60907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0007242; F:lntracellular signaling cascade; IEA.
InterPro; IPR01054; G_cyclase.
Ffam; PF00211; Guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                               596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  675 AA; 75498 MW; E71A283DC0369601 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble guanylyl cyclase alphal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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90.0%; Pred. No. 8.6;
live 0; Mismatches
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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                         Biochim. Biophys. Acta 1086:326-334 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                        transcriptional regulation.
                                                                                                                                                            EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                                                                      Local Similarity 90.0
es 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     226 TŘĽŤŘKRČĽK 235
                                                                                                                                                                                                                                            296
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es 8; Conserv
                                                                                SEQUENCE FROM N.A.
TISSUE=Liver;
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596
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NON_TER 59
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090VV5 Q90VV5;

RESULT 3

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Best Loc Matches

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P79997; P79997

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RESULT 4

Best Loc Matches

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DNA 6:363-372(1987).
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                                                        SEQUENCE
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Wikami T., Kusakabe T., Suzuki N.;
Mikami T., Kusakabe T., Suzuki N.;
Mikami T., Kusakabe T., Suzuki N.;
Tandem organization of medaka fish soluble guanylyl cylclase alphal
T and betal subunit genes ";
T two subunit genes subunit genes ";
T two subunit genes s
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CarlBason P., Darnfors C., Olofsson S.O., Bjursell G.;
CarlBason P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of
the B-74 region.";
Gene 49:29-51 (1986).
Gene, M15421; AAS1758.1; -.
                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 14, Last annotation update)
Soluble guanyly cyclase alpha subunit.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Last annotation update)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2;
Pred. No. 9.9;
1; Mismatches
                                                                                                                                                                                                 678 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                              PRT;
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013788;
01-007-1996 (TrEMBLrel. 01, Ca
01-NOV-1996 (TrEMBLrel. 01, La
01-JUN-2003 (TrEMBLrel. 24, La
APOB protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 RLTRKDGLR 324
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316 RLTRKDGLR 324
RLTRKDGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8090;
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                                                                                                                                                                                                                               09PWI2;
                                                                                                                                                                                              Q9PWI2
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                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy Wilson B., Scott J.,
"Complete cDNA and derived protein sequence of human apolipoprotein B-
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                                                                                                                                                                                                       Gaps
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P04114; 000502; Q13787;
01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
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MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li
Gotto A.M. Jr., Chan L.;
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Zannis V.I.;
                                                                                                                                        DB 2; Length 3262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE=88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Piecrti V.R., Caiati L., For'
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy I
"DNA sequence of the human apolipoprotein B gene.";
                                                                            56603BC0618DD40D CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986)
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MEDLINE=85270450; PubMed=3860836;
Deeb S.S., Motulaky A.G., Albers J.J.;
"A partial CDNA clone for human apolipoprotein B Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
                                                                                                                                    Score 42; DB 2
Pred. No. 56;
0; Mismatches
GO; GO:0006869; P:lipid transport; NAS.
NON TER 1 1
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J. Biol. Chem. 261:12918-12921(1986).
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                                                                         3262 AA; 370140 MW;
                                                                                                                                    Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Query Match
     [10]
SEQUENCE OF 1-291 FROM N.A.
SEQUENCE OF 1-291 FROM N.A.
MEDLINE-86149325; PubMed=3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., Mosnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr., Innersatity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R., Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J., "Complete protein sequence and identification of structural domains of human apolipoprotein B.";
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                                                                                                                                                                                                                                                                                                     carboxyl-terminal domains, sites
             MEDLINE-86041888; PubMed=3903660; Mest R., Johnson D.F., Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F., Kirchgesner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.; Human apolipoprotein B: identification of cDNA clones and characterization of mRNA.; Nucleic Acids Res. 13:6937-6953(1985).
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kai H., Byers M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-848.
MEDLIAE-88018019; PubMeda=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Dealypere J.P., Rosseneu M.,
Gotto A.M., Dr., Li W.-H., Chan L.;
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specific in-frame stop codon.";
                                                                                                             SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
MEDLINE-86093680; PubMed-3841204;
                                                                                                                                                                                                          SEQUENCE OF 3109-4563 FROM N.A.

MEDLINE=85300528; PubMed=2994225;

Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M..

Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.

Priestley L.M., Robertson B., Rall L.B., Betsholtz C., Shows T.B.,

Mahley R.W., Scott J.;

"Human apolipoprote of B. structure of carboxyl-terminal domains, si
of gene expression, and chromosomal localization.";
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"Analysis of CDNA clones encoding the entire B-26 region of human apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
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                                                                                                                                         Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund Bjursell G.,
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Nucleic Acids Res. 13:8813-8826(1985).
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MEDLINE-86287319; PubMed=3461454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific in-frame stop codon.";
Science 238:363-366(1987).
 OF 3056-3159 FROM N.A.
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"Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100."; Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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MEDLINE=91071750; PubMed=1979313;
Mavajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
Cunny G., Cambien F., Roizes G.;
"Detection by denaturing gradient gel electrophoresis of a new
polymorphism in the apolipoprotein B gene.";
"Hum. Genet. 86:91-93(1990).
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Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene
PCR-SSCP.";
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MEDIJIBE-89908975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
                           MEDLINE=20143590; PubMed=10679026;
Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper
intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  simultaneous
mutations in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND ILE-3921.
MEDLINE-98141125, PubMed=9490296,
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
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Hum. Genet. 102:44-49(1998).
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MEDLINE=97403938; PubMed=9259199;
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MEDLINE-95190020; PubMed=7883971;
                                                                                                                                                                                                                     11:721-734 (2000)
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PALMITOYLATION OF CYS-1112
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                                                                                                                                                                                                                     Biol. Cell
                                                                                                                                                                                      triglycerides.
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Gaps

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Similarity 90.0%; Pred. No. 81; Length 4563; 9; Conservative 0; Mismatches 1; Indels

Local Similarity

Matches

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89
89 AA;
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SEQUENCE
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EMBL; AF132072; AA736517.1; -.

PIR; A60225, A60225.

HSSP; P08559; INI4.

GO; GO:0016624; F:oxidoreductase activity, acting on the alde. . .; IEA.

GO; GO:008152; P:metabolism; IEA.

InterPro; IFR001017; Dehydrogenase_E1.

Pfam; PF00676; E1_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 26, Last annotation update)
Pyruvate dehydrogenase El component alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2; Length 4563;
Pred. No. 81;
0; Mismatches 1; Indels
                                                                                                                                                                                                            Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
                                                                                                                                                                                                                               Nickerson D.A.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                EMBL, AY324608, AA772970.1;
GO; GO:0005319; F:lipid transporter activity; IEA.
GO; GO:0005869; P:lipid transport; IEA.
Interpro; IPR009454; DUF1081.
Interpro; IPR001747; Lipid transprt_N.
Pfam; PF06448; DUF1081; 1.
Pfam; PF01347; Vitellogenin_N; 1.
                                                                             4563 AA.
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                            3385 TRLTRKRGLK 3394
                                                                             PRELIMINARY;
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         TRLTRKDGLK 10
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SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=9606;
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Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
E9C7DF85389A47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overall
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pucleic Acids Res. 18:4925-4925(1990).

**Included Acids Res. 18:4925-4925(1990).

-!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overa conversion of pyruvate to acety!—CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

-!- CATALYTIC ACTIVITY: Pyruvate + (dihydrolipoyllysine-residue acetyltransferase) S-acetyldihydrolipoyllysine + CO(2).

-!- COFACTOR: Thiamine pyrophosphate.

-!- COFACTOR: Thiamine pyrophosphate.

-!- ENZYME REGULATION: El activity is regulated by phosphorylation (inactivation) and dephosphorylation (activation) of the alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sermon K., Demeirleir L., Elpers I., Lissens W., Liebaers I., "Characterisation of a cDNA for porcine PDH-E1 alpha and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (P1g).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
95-JUL-2004 (Rel. 41, Last annotation update)
mitochondrial precursor (EC 1.2.4.1) (PDHEL-A type I) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit.
SUBUNIT: Tetramer of two alpha and two beta subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00676; El_dh; 1. Panydrogenase_El.
Blavoprotein; Glycolysis; Mitochondrion; Oxidoreductase; Phosphorylation; Thiamine pyrophosphate; Transit peptide.
NON TER <1 28 Mitochondria.
                                                          Length 89;
                                                                                                                       1; Indels
10293 MW; B47759C2D169292B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                       Score 38; DB 2;
Pred. No. 7.3;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                     389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X52990; CAA37180.1; -.
PIR; S20813; DEPGPA.
HSSP; P08559; INI4.
InterPro; IPR001017; Dehydrogenase_E1.
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                  80.08;
                                                             76.08;
                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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389
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45 TVLTREDGLK 54
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292
299
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292
299
389 AA;
                                                       Query Match
Best Local Similarity
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FROM
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SEQUENCE FROM N.A.
MEDLINE=89315791; PubMed=2748588;
MEDLINE=89315791; PubMed=2748588;
HO L., Wexler I.D., Liu T.C., Thekkumkara T.J., Patel M.S.;
HO L., Wexler I.D., Ciu T.C., Thekkumkara T.J., Patel M.S.;
"Characterization of cDNAs encoding human pyruvate dehydrogenase alpha"
"Characterization of cDNAs encoding human pyruvate dehydrogenase alpha
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahl H.-H.M., Hunt S.M., Hutchison W.M., Brown G.K.,
"The human pyruvate dehydrogenase complex. Isolation of cDNA clones
for the El alpha subunit, sequence analysis, and characterization of
the MRNA.";
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MEDLINE-88124815; PubMed=3422424;
Koike K., Ohta S., Urata Y., Kagawa Y., Koike M.;
"Cloning and sequencing of CDNAs encoding alpha and beta subunits of human pyruvate dehydrogenase.";
Proc. Natl. Acad. Sci. U.S.A. 85:41-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Brown G.K., Dahl H.-H.M.;
the El alpha subunit of the
                                                                                                                                                                                                                                                                                      TISSUE=Leukocyte;
MEDLINE=91033044; PubMed=2227443;
MCDLINE=91033044; PubMed=2227443;
MCDLINE=91033044; PubMed=2227443;
"Characterization and nucleotide sequence of the gene encoding the human pyruvate dehydrogenase alpha-subunit.";
Gene 93:307-311(1990).
                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                         ODPA HUMAN STANDARD; PKI; 350 Am.
ODBSES, ODNP12;
01-AUG-1998 (Rel. 02, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Pyruvate dehydrogenase El component alpha subunit, somatic form, mitochondrial precursor (EC 1.2.4.1) (PDHEL-A type I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human El
                           ;
    Length 389
                           1; Indels
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MEDLINE=88115327; PubMed=2828359;
de Meirleir L., MacKay N., Wah A.M.L.H., Robinson B.H.;
"Isolation of a full-length complementary DNA coding for alpha subunit of the pyruvate dehydrogenase complex.";
J. Biol. Chem. 263:1991-1995(1988).
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TISSUE=Brain, and Liver;
Huh T.L., Chi Y.T., Casazza J.P., Veech R.L., Song B.J.;
Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases.
   DB 1,
                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89308653; PubMed-2745444;
Maragos C., Hutchinson W.M., Hayasaki K.,
"Structural organization of the gene for thuman pyruvate dehydrogenase complex.";
J. Biol. Chem. 264:12294-12298(1989)
  Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 262:7398-7403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87222349; PubMed=3034892;
Dahl H.-H.M., Hunt S.M., Hutchigor
 76.0%;
                        8; Conservative
                                                           | |||:||||
53 TVLTREDGLK 62
                                               1 TRLTRKDGLK 10
                                                                                                                                                                                                                      Homo sapiens (Human)
             Local Similarity
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
Query Match
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                                                                                                     RESULT 12
ODPA_HUMAN
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Matches
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A MEDLINE=22388257; PubbMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausper R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunzarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Louchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U.S. Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
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"Mutexions in the X.1Inked El alpha subunit of pyruvate dehydrogenase
leading to deficiency of the pyruvate dehydrogenase complex.";
Hum. Mol. Genet. 2:449-451(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVIEW ON VARIANTS.
MEDIATE-924485; PubMed=1301207;
Dahl H.-H.M., Brown G.K., Brown R.M., Hansen L.L., Kerr D.S.,
Wexler I.D., Patel M.S., de Meirleir L., Lissens W., Chun K.,
McKay N., Robinson B.H.;
"Mutations and polymorphisms in the pyruvate dehydrogenase El alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "X-linked pyruvate dehydrogenase El alpha subunit deficiency in heterozygous females: variable manifestation of the same mutation."; J. Inherit. Metab. Dis. 15:835-847(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT PDHEL DEFICIENCY LYS-313 DEL, AND VARIANT LS HIS-378. MEDLINE-91359689; Pubmed=1900401; Hansen L.L., Brown G.K., Kirby D.M., Dahl H.-H.M.; "Characterization of the mutations in three patients with pyruvate dehydrogenase El alpha deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic characterization of an X-linked form of Leigh's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARTANT LS ALA-258.
MEDLINE-93270474; PubMed=8458846;
Matthews P.M., Marchington D.R., Squier M., Land J., Brown R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS PDHE1 DEFICIENCY MET-167; THR-199; ALA-231; GLY-263 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahl H.-H.M., Hansen L.L., Brown R.M., Danks D.M., Rogers J.G.,
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MEDLINE=94258164; PubMed=8199595;
Dahl H.-H.M., Brown G.K.;
"Pyruvate dehydrogenase deficiency in a male caused by a point mutation (F2051) in the El alpha subunit.";
Hum. Mutat. 3:152-155(1994).
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MEDLINE=93188402; PubMed=1293379;
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VARIANT PDHE1 DEPICIENCY GLN-263.
MEDLINE=95056975; PubMed=7967473;
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Chun K., MacKay N., Petrova-Bendict R., Federico A., Fois A., Cole D.E.C., Robertson E., Robinson B.H.; "Mutations in the X-linked El alpha subunit of pyruvate dehydrogenase: exon skipping, insertion of duplicate sequence, and missense mutations leading to the deficiency of the pyruvate dehydrogenase complex."; Am. J. Hum. Genet. 56:558-569(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1) dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).
-- CARIATYTIC ACTIVITY: Pyruvate + [dihydrolipoyllygine-residue acetyltransferase] lipoyllygine = [dihydrolipoyllygine-residue acetyltransferase] Sacetyldhydrolipoyllysine + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9276751, PubMed=7757088;
Hemalatha S.G., Kerr D.S., Wexler I.D., Lusk M.M., Kaung M., Du Y.,
Kolli M., Schelper R.L., Patel M.S.;
"Pytuvate dehydrogenase complex deficiency due to a point mutation
(P188L) within the thiamine pyrophosphate binding loop of the El alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS PDHEI DEFICIENCY CYS-302 AND HIS-302.
MEDLINE=98334347; PubMed=9671272;
Otero L.J., Brown R.W., Brown G.K.;
"Arginine 302 mutations in the pyruvate dehydrogenase Elalpha subunit gene: identification of further patients and in vitro demonstration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lissens W., de Meirleir L., Seneca S., Benelli C., Maraac C.,
Poll-The B.T., Briones P., Ruitenbeek W., van Diggelen O., Chaigne D.,
Ramaekers V., Liebaers I.;
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"An amino acid substitution in the pyruvate dehydrogenase El alpha gene, affecting mitochondrial import of the precursor protein.";
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alpha gene from two boys with primary lactic acidaemia.";
J. Inherit. Metab. Dis. 17:189-195(1994).
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Tripatara A., Kerr D.S., Lusk M.M., Kolli M., Tan J., Patel M.S.;
Tripatara A., Kerr D.S., Lusk M.M., Kolli M., Tan J., Patel M.S.;
Tribre new mutations of the pyruvate dehydrogenase alpha subunit:
point mutation (M181V), 3 bp deletion (-R282), and 16 bp
insertion/frameshift (K3588VS->TVDQS).";
Hum. Mutat. 8:180-182(1996).
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                                                                                                                  VARIANTS PDHE1 DEFICIENCY CYS-72; GLY-263 AND ARG-311 DEL, AND
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                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96029268; PubMed=7573035;
                                                                                                                                        VARIANTS LS LEU-205 AND HIS-378,
MEDLINE=95193781; PubMed=7887409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit.";
Hum. Mol. Genet. 4:315-318(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96263737; PubMed=8664900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogenicity.";
Hum. Mutat. 12:114-121(1998)
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                                                                                                                                                                                                                                                                                                                                          overall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                 Fitzgerald G.F., Hutchison W.M., Dahl H.H.M., \  \,  "Isolation and characterisation of the mouse pyruvate dehydrogenase
                                                                                                                                                                                                                                                                                                                Blochim. Blophys. Acta 1131:83-90(1992).

-I-FUNCTION: The pyruvate dehydrogenase complex catalyzes the overa conversation of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).

-I-CATALYTIC ACTIVITY: Pyruvate + [dihydrolipoyllysine-residue acetyltransferase] lipoyllysine = [dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine + CO(2).

-I-CORATOR: Thiamine pyrophosphate.

-I-CORATOR: Thiamine pyrophosphate.

-I-CORATOR: Thiamine pyrophosphate.

-I-ENXYME REGULATION: El activity is regulated by phosphorylation (inactivation) of the alpha
                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Tetramer of two alpha and two beta subunits.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- TISSUE SPECIFICITY: In all tissues, but in very low amount in
                                                                                           somatic form,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (By similarity)
Phosphoserine (By similarity)
Phosphoserine (By similarity)
A0898944CE8E0A03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 390;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Phosphorylation; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P08559; INI4.
MGD; MGI:97532; Pdhal.
GO; GO:0004738; F:pyruvate dehydrogenase activity; IMP.
InterPro; IPR001017; Dehydrogenase_E1.
                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annoteation update)
Pyruvate dehydrogenase El component alpha subunit,
mitochondrial precursor (EC 1.2.4.1) (PDHEI-A type
Name-Pdha1; Synonyms-Pdha-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                MEDLINE=92256495; PubMed=1581363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43231 MW;
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PIR; S23506; S23506.
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80.0%;
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 AA;
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                                                                                                                                                                                            NCBI_TaxID=10090;
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ODPA MOUSE
P35486;
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Best Local S
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Gaps

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Indels

DB 1; Length 390;

Score 38; DB 1 Pred. No. 37; 1; Mismatches

76.0%; 80.0%;

Query Match Best Local Similarity

8; Conservative 1 TRLTRKDGLK 10 | |||:|||| 54 TVLTREDGLK 63

Matches

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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion (By similarity).

Pyruvate dehydrogenase El component alpha subunit, somatic form.

Phosphoserine (By similarity).

Phosphoserine (By similarity).
                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91223087; PubMed=2025639;
Matuda S., Nakano K., Ohta S., Saheki T., Kawanishi Y., Miyata T.;
"The alpha-ketoacid dehydrogenase complexes. Sequence similarity of
rat pyruvate dehydrogenase with Escherichia coli and Azotobacter
vinelandii alpha-ketoglutarate dehydrogenase.";
Biochim. Blophys. Acta 1089:1-7(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit.
-!- SUBUNIT: Tetramer of two alpha and two beta subunits.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- TISSUE SPECIFICITY: In all tissues, but in very low amount in
                                                                        01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pyruvate dehydrogenase El component alpha subunit, somatic form,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00676; Bl_dh; 1.
Flavoprotein, Glycolysis, Mitochondrion; Multigene family;
Oxidoreductase; Phosphorylation; Thiamine pyrophosphate;
                                                                                                        tochondrial precursor (EC 1.2.4.1) (PDHE1-A type I).
                                          390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z12158; CAA78146.1; -.
PIR; S15891; DERTPA.
PIR; S21553; DERTP1.
PSP; P08559; INI4.
RGD; 3286; Pdhal.
InterPro; IPR001017; Dehydrogenase_El.
                                          PRT;
                                                               Created)
                                          STANDARD;
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390
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                                                              01-MAY-1992
                                                                                                                 Name=Pdha1;
                                                                       01-MAY-1992
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016624; F:oxidoreductase activity, acting on the alde. GO; GO:008152; P:metabolism; IRA. InterPro; IPR001017; Dehydrogenase_E1. PFR00676; E1_dh; 1.
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300 Phosphoserine (By similarity).
10 R -> H (in Ref. 2).
126 N -> T (in Ref. 2).
130 H -> LP (in Ref. 2).
134 V -> I (in Ref. 2).
43212 MW, 21B78A8014460DC0 CRC64;
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                                                                                                                              Score 38; DB 1; Length 390;
Pred. No. 37;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=Brain cerebellum cortex; Kusuda J., Osada N., Hida M., Sugano S., Hashimoto K.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 AA; 43365 MW; 420CE38364BDB33C CRC64;
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Job time : 80.0328 secs
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80.0%;
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HSSP; P08559; 1NI4.
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Beet Local Similarity 80.00,
Beet Local Similarity 80.00,
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NCBI_TaxID=9541;
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54 TVLTREDGLK 63
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RESULT 1
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Aay30693 Apo-B100
Aaw57205 Apo B bin
Aaw57207 Apo B 100
Aaw41261 Apolipopr
Aaw96892 ApoB-100
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                                                                                           January 13, 2005, 01:14:40 ; Search time 77.2131 Seconds (without alignments) 46.460 Million cell updates/sec
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version 5.1.6
- 2005 Compugen Ltd.
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Listing first 45 summaries
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Match 1
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56	44	89.8	4563	9	ABU79140	Abu79140	Apolipopr
27	44	6	4563	7	ADF43408	Adf43408	Apolipopr
28	44	89.8	4563	æ	ADH18871	Adh18871	Human abo
53	44		4563	œ	ADH18870	Adh18870	Human apo
30	44	٩.	4563	œ	AD033445	Ado33445	
31	44		4563	œ	AD033447	Ado33447	
32	44	8.68	4590	4	AAU33184	Aau33184	Novel hum
	41	83.7	465	4	AAB92994	Aab92994	Human pro
34	41	83.7	709	4	AAB95320	Aab95320	Human pro
32	41	83.7	719	,	ADM36086	Adm36086	Human acy
36	41	83.7	720	ო	AAY94296	Aay94296	Human coe
37	41	83.7	720	ഹ	ABG61883	Abg61883	Prostate
38	41	83.7	720	9	ABR63871	Abr63871	Human Fac
39	41	83.7	720	7	ADE31735	Ade31735	
40	41	83.7	720	7	ADN95365	Adn95365	Human BEC
41	41	83.7	720	8	ADJ45487	Adj45487	LXR-ligan
42	41	83.7	720	8	ADP05461	Adp05461	Human ace
43	40	81.6	10	N	AAY30682		Apo-B100
44	40	81.6	10	N	AAY30687	Aay30687	Apo-B100
45	39	9.62	10	N	AAY30690	_	Apo-B100

ALIGNMENTS

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. AAY30692 standard; peptide; 10 AA 98US-0077618P. 99WO-US004805. Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Homo sapiens 05-MAR-1999; WO9946598-A1 10-MAR-1998; 17-NOV-1999 16-SEP-1999 Synthetic AAY30692; AAY30692

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method camprises detecting compounds which affect in building LDL receptor binding with compounds can be used for identifying compounds which compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Human Pro Human apo Human ali

AAO15893 ABR40253

4561 4563 4563

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Sequence 10 AA;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atheroselerosels. The peptides are derived from anino acids 3158 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method computes detecting LDL-PG binding with broteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent can be used to atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo assay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in catheroselerotic regions. Thus the assays may be used to determine whether compounds to atheroselerotic lesions. Thus the assays may be used to determine whether formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerotic lesions or mammal
                 atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo-B100, proteoglycan receptor mutation, atherosclerosis,
low density lipoprotein, proteoglycan, LDL, atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-B100 derived peptide showing a proteoglycan receptor mutation.
  also be used to identify compounds which result in an increase in
                                                                                                                                                                                 100.0%; Score 49; DB 2; Length 10; 100.0%; Pred. No. 0.0095; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           AAY30693 standard; peptide; 10 AA.
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                            Sequence 10 AA;
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Matches
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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKNKHRH (1) or THRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) crug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                    Gaps
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 93.9%; Score 46; DB 2; Length 10; 90.0%; Pred. No. 0.037;
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90.0%; Pred. No. 0.1;
iive 0; Mismatches
                                  1; Mismatches
                                                                                                                                                                                   AAW57205 standard, peptide; 11 AA.
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                                                                                                                                                                                                                                                                                  Apo B binding site peptide 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that express this receptor.
                                                                                                                                                                                                                                                   (first entry)
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYST ) UNIV STRATHCLYDE.
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                                                                 1 TELTRKRGLK 10
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TDLTRKRGLK 10
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TRLTRKRGLK 11
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               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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Query Match
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                               Matches
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(first entry)
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               19-MAY-1998
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                                                                                                                                                              Synthetic
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ZXEXEXEX & X &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-tazgeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete app B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                        Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
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                                                                                                                                                                                                                                                                                                            'note= "attached to retinoic acid"
                                                                                                                                           Apo B 100 binding site peptide analogue peptide B.
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affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                          AAW57207 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor – useful as, e.g. <sup>,</sup>
that express this receptor.
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halbert GW, Owens MD,
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Modified-site
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                                                                           AAW57207;
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                           AAW57207
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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apol-100). IL-KAQ-XI-KUKURHSHS-X2-T-Z2 (I) XI = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, or 1-47 amino acids or Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent processes, specifically to prevent or reduce blood coagulation (e.g. curing or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits active as such or as part of a 98-aa peptide, inhibits activation of the prothrombinase complex; and prevents activation of activation of the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                        Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0; Mismatches
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Apolipoprotein B-100 fragment.
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Query Match
Best Local Similarity 90.uv,
Best Local Similarity
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20-JUL-2001; 2001US-0306726P.
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Best Local Similarity
                                                                                                                                                                                                                                                  Sequence 20 AA;
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Modified-site
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                                                           Hubbell JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                          AAW57208;
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                RESULT 8
         à
                                                                                                                                                                                                                                                                                                                                  요
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                           human apolipoprotein B-100 (appB-100). AppB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoprotein a. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic calls, in wirro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                      Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                  AAW96878-97 represent nuclear localisation signal sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2; Length 15;
Pred. No. 0.14;
0; Mismatches 1; Indels
                                                                                                                                                                              Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin binding peptide sequence #28
                                                                                                                                                                                                                                                              Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                          98WO-US011927
                                                                                                                            97US-00874807.
                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TELTRKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rkirkkeik 15
                                                                                                                                                                                                   WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003007689-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                           Homo sapiens
                                                                W09856938-A1
                                                                                                       10-JUN-1998;
                                                                                                                            13-JUN-1997;
                                                                                                                                       14-MAY-1998;
                                                                                   17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003
                                                                                                                                                                                                                                            treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ37575;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                            Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide binding to apo B protein delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 6; Length 20;
Pred. No. 0.18;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'notes "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "attached to cholesterol"
  Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
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                                                                                                                                                                                                         Disclosure; Fig 2; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57208 standard; peptide, 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%;
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Schoenmakers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
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7 TRLTRKRGLK 16
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKNKHRH (1) or TTRLFKRRGEK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives courring, receptor-competent LDL particles are corring, receptor-competent LDL particles are corring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                           Score 44; DB 2; Length 22; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57209 standard; peptide; 22 AA.
           Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                           89.8%;
90.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                   1 TELTRKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                      TRLTRKRGLK
                                                                                                                                                                                                                                                                                                         Local Similarity
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Modified-site
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                                                                                                                                                                                                                                                                Sequence 22
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Matches
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Gaps .; 0

1; Indels

Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site. Apo B 100 binding site peptide analogue peptide D. /note= "attached to retinoic acid"

Baillie G; Owens MD, WPI; 1998-230637/20. Halbert GW,

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Claim 13; Fig 7; 73pp; English.

The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

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0
particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                           2; Length 22;
                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                           Score 44; DB 2
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE14541 standard; peptide; 34 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-2000; 2000GB-00017641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARKT-) ARK THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                           89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         7 TRLTRKRGLK 16
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                                                                                                                                                                                                                                                        Sequence 22 AA;
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Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                                                                      Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                                                                                                                                                             Human apolipoprotein peptide fragment #1.
                                                                           AAW64587 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                  98EP-00890007
                                                                                                                                                                                                                                                                                                                                                                             97AT-00000044
                                                                                                                                 (first entry)
       11 TRLTRKRGLK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-416142/36.
                                                                                                                                                                                                                                                                                                                                                                                                        (IMMO ) IMMUNO AG.
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                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                  23-OCT-1998
                                                                                                                                                                                                                                                                                                                                               12-JAN-1998;
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                                                                                                      AAW64587;
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                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                           Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollipoprotein; binding; in vivo transport; nucleic acid; binding donain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                               Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                        Length 34;
                                                                                                   1; Indels
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                                                                        DB 5;
                                                                                      0.31;
                                                                       Score 44; DB 5
Pred. No. 0.31;
0; Mismatches
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                                                                                                                                                                                                                             AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoogeveen RC, Moore
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                                                                     89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers (particularly non-sma.
fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00874807.
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                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                   9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                   Sest Local Similarity
Astches 9; Conser
                                            Sequence 34 AA;
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                                                                                                                                                                                                                                                                                     22-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment.
                                                                                                                                                                                                                                                         AAW96876;
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                                                                       Query Match
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Schenk V;

Lang H,

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                                                                                                                                                                                                                                                                                                                                                                                                                      mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is particularly suited to routine screening. It also allows mutant protein
AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apoE indicates increased risk of developing Alzheimer's disease), thermostable 5,10-methylenetetrahydrofolate reductase (associated with hypercysteinaemia and venous thrombosis) and factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 2;
Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW96845 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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ID AAW9
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Conservative

1 TELTRKRGLK 10

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Gaps

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04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                           Chen W,
                                                                                 2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                  21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178
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                                                                                                                                                                                          Hanzel DK,
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                                                                                                                                                                                                                  WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TELTRKRGLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
  WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157273-A2
                                                                                            30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                      04-FEB-2000;
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                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG52504;
                                                                                                                                                                                          Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The sequence can be used in the composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapoutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                             Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                bound to LDL or VLDL lipoprotein - cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 51;
Pred. No. 0.46;
0; Mismatches 1; Indels
                                                        Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                  Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                              Composition comprising nucleic acid used for delivering nucleic acid to
                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB37687 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                  98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.8%;
                                                                                                                                                                                                               98WO-US011927
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                                 22-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                        WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51 AA;
                                                                                                                                          Homo sapiens
                                                                                                                                                                WO9856938-A1
                                                                                                                                                                                                               10-JUN-1998;
                                                                                                                                                                                                                                       13-JUN-1997;
                                                                                                                                                                                                                                                  14-MAY-1998;
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                                                                                                                                                                                        17-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                       treatment.
           AAW96845;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
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                                                                           DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 31152.
                                                                               Rank
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(MOLE-) MOLECULAR DYNAMICS INC
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(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is ascalated with coronary heart disease. ABG47748-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences Claim 27; SEQ ID NO 31152; 658pp; English.

Sequence 343 AA;

Gaps ö 89.8%; Score 44; DB 4; Length 343; 90.0%; Pred. No. 3.1; .ive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9, Conservative

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1 TELTRKRGLK 10 ò

| ||||||| 169 TRLTRKRGLK 178 g

Search completed: January 13, 2005, 01:43:01 Job time : 78.3798 secs

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Appli

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24, Appl
28, Appl
2, Appli
10596, A
10595, A
                                                                                                                                                                   26, Appl
30, Appl
4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4754, Ap
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0
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APPLICANT: Spencer, Brian
IIILE OF INVENTION: Compositions and Methods For Targeting a
IIILE OF INVENTION: Polypeptide To the Central Nervous System
FILE REFERENCE: 66671-131
CURRENT APPLICATION NUMBER: US/10/861,779
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,482
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.8%; Score 44; DB 8; Length 3000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Score 44; DB 6; Length 42; 90.0%; Pred. No. 0.066; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOSELOFF, Elizabeth et al.
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001568
CURRENT APPLICATION NUMBER: US/60/636,722
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 2719
SEC ID NO 924
LENGTH: 3000
US-10-999-233-18
US-10-999-233-16
US-10-999-233-20
US-10-999-233-20
US-10-732-923-3311
US-10-408-765-2504
US-10-999-233-26
US-10-999-233-24
US-10-999-233-24
US-10-999-233-28
US-10-999-233-28
US-10-999-233-28
US-10-999-233-28
US-10-999-233-28
US-10-999-233-28
US-10-999-233-28
US-10-999-238-10595
US-10-990-328-10595
US-10-990-328-10595
US-10-990-328-10597
US-10-950-328-10597
US-10-990-328-10597
US-10-950-328-10597
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US-60-636-722-924
Sequence 924, Application US/60636722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-861-779-1; Sequence 1, Application US/10861779; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                       1 TELTRKRGLK 10
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-60-636-722-924
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16 TRLTRKRGLK
                                                    US-10-861-779-1
       LENGTH: 42
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Sequence 924, App
Sequence 2, Appli
Sequence 25, Appli
Sequence 919, App
Sequence 919, App
Sequence 921, App
Sequence 925, App
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Sequence 279, App
Sequence 280, App
Sequence 281, App
Sequence 282, App
Sequence 283, App
Sequence 2245, App
Sequence 2245, App
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Sequence 11685, A
Sequence 11686, A
Sequence 11687, A
Sequence 11688, A
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Sequence 16246, i
Sequence 65100, i
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                                                                                                                                                         January 13, 2005, 01:43:16; Search time 10.6557 Seconds (without alignments) 47.947 Million cell updates/sec
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1: /cgn2 6/ptodata/1/paa/PCT NEW COMB.pep:*
2: /cgn2 6/ptodata/1/paa/USO6 NEW COMB.pep:*
3: /cgn2 6/ptodata/1/paa/USO7 NEW COMB.pep:*
4: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*
5: /cgn2 6/ptodata/1/paa/USO8 NEW COMB.pep:*
6: /cgn2 6/ptodata/1/paa/USI0 NEW COMB.pep:*
7: /cgn2 6/ptodata/1/paa/USI1 NEW COMB.pep:*
8: /cgn2 6/ptodata/1/paa/USI1 NEW COMB.pep:*
                        version 5.1.6
- 2005 Compugen Ltd.
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US-60-636-722-924
US-60-636-722-923
US-10-398-200-2
US-10-398-200-2
US-60-636-722-919
US-60-636-722-921
US-60-636-722-922
US-60-636-722-922
US-10-990-328-11686
US-10-990-328-11686
US-10-990-328-11688
US-60-636-720-289
US-10-773-923-16259
US-10-732-923-16259
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                        GenCore (c) 1993
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Maximum DB seq length: 2000000000
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49
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                                                                                                                                                                                                                                                                                                              Sequence:
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; ORGANISM: Homo sapiens
US-60-636-722-921
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                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                         FEATURE:
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GENERAL INFORMATION:
Harry Adversal Conversed of Flatter of Invention of Intle OF Invention:
TITLE OF INVENTION: ELAVIVIRIDAE VIRUSES, AND ANY OTHER VIRUS THAT
TITLE OF INVENTION: COMPLEXES TO LOW DENSITY LIPOPROTEIN OR TO VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROCEIN IN BLOOD BY PREVENTING VIRAL ENTRY
TITLE OF INVENTION: INTO A CELL
FILE REFERENCE: 1513-PCT-00
CURRENT APPLICATION NUMBER: 0210/398,200
CURRENT PILING DATE: 2003-04-03
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE PARENTIN VET. 2.1
SEQ ID NO 2
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                                                                                                                                                                           Sequence 323-323

; Sequence 323-323

; GENERAL INFORMATION:

APPLICANT: JOSELOFF, Elizabeth et al.

; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF;

; FILE REFERENCE: CLO01568

; CURRENT APPLICATION NUMBER: US/60/636,722

; NUMBER OF SEQ ID NOS: 2719

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 923

LERGIN: 3262
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                   1; Indels
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GENERAL INFORMATION:
APPLICANT: Alitalo et al.
TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28967/39359A
90.0%; Pred. No. 5.3;
                 0; Mismatches
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Best Local Similarity 90.07
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Best Local Similarity 90.0
Matches 9; Conservative
               9; Conservative
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; ORGANISM: Homo sapiens
US-60-636-722-923
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Best Local Similarity
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-10-398-200-2
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US-60-636-722-919
Sequence 919, Application US/60636722
Sequence 919, Application US/60636722
GENERAL INFORMATION:
APPLICANT: JOSELOFF, Elizabeth et al.
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF;
FILE REFERENCE: CLO01568
CURRENT APPLICATION NUMBER: US/60/636,722
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 2719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 919
LENOTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.8%; Score 44; DB 6; Length 4563; 90.0%; Pred. No. 8.1;
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GENERAL INFORMATION:
APPLICANT: JOSELOF,
ITILE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF;
FILE REFERENCE: CLO01568
CURRENT PAPLICATION NUMBER: US/60/636,722
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 2719
SEQ ID NOS: 2719
SEQ ID NO 921
LENGTH: 4563
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Pred. No. 8.1;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/868,577A;
CURRENT FILING DATE: 2004-06-14;
PRIOR APPLICATION NUMBER: US 60/478,390;
PRIOR FILING DATE: 2003-06-12;
PRIOR PLING DATE: 2003-09-23;
NUMBER OF SEQ ID NOS: 69;
SOFTWARE: Patentin version 3.2;
LENGTH: 4563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (32)...(126)
OTHER INFORMATION: heparin binding domain
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

LOCATION: (3161).. (3236)

COTHER INFORMATION: heparin binding domain

US-10-868-5778-25
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90.0%;
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Best Local Similarity 90.00,
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: BOCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001495
CURRENT APPLICATION NUMBER: US/10/990,328
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11687
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                         Sequence 11686, Application US/10990328
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: DOLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE REPRENCE: CLOOL495
CURRENT APPLICATION NUMBER: US/10/990,328
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FBASESQ for Windows Version 4.0
SEQ ID NO 11686
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Pred. No. 4.7;
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Pred. No. 4.7;
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NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11685
LENGTH: 720
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; APPLICANT: CARGILL, Michele
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80.0%;
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Best Local Similarity 80.0.
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Matches 8; Conservative
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633 TELARKKGLK 642
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633 TELARKKGLK 642
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                                                                             TYPE: PRT; ORGANISM: Homo sapiens
US-10-990-328-11685
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-990-328-11687
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nes 8; Conserv
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
TITLE REFERENCE: CLO01495
CURRENT APPLICATION NUMBER: US/10/990,328
CURRENT FILING DATE: 2004-11-17
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GENERAL INFORMATION:
APPLICANT: JOSELOFF, Elizabeth et al.
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF;
FILE REPERENCE: CLO01568;
CURRENT FILING DATE: 2004-12-17;
NUMBER OF SEQ ID NOS: 2719
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 925.
                        DB 8; Length 4563;
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Sequence 922, Application US/60636722
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/636,722
CURRENT FILING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 2719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 922
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Pred. No. 8.1;
0; Mismatches
                      Score 44; DB (Pred. No. 8.1; 0); Mismatches
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                    89.8%;
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-636-722-922
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CORGANISM: Homo sapiens
US-60-636-722-925
                  Query Match
Best Local Similarity
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US-60-636-722-925
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Gaps

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Gaps

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Sequence 11688, Application US/10990328
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYWORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNDER: 2004-11-17
NUMBER OF SEQ ID NOS: 558034
SOFTWARE: FRANCESC for Windows Version 4.0
SEQ ID NO 11688
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APPLICANT: DOMON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF; TITLE OF INVENTION WHERE: US/60/636,720; CURRENT FILING DATE: 2004-12-17; NUMBER OF SEQ ID NOS: 4325; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 278
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                     83.7%; Score 41; DB 6; Length 720; 80.0%; Pred. No. 4.7; ive 1; Mismatches 1; Indels
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83.7%; Score 41; DB 8; Length 720;
Best Local Similarity 80.0%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: DOMON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001567
CURRENT PELLING DATE: 2004-12-17
NUMBER OF SEQ ID NOS: 4325
SOFTWARE: Fallse for Windows Version 4.0
EDGTH: 720
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 TELARKKGLK 642
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                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-990-328-11688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-636-720-278
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; ORGANISM: Homo sapiens
US-60-636-720-279
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Best Local Similarity
US-10-990-328-11688
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US-60-636-720-279
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GenCore version 5.1.6
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- protein search, using sw model OM protein January 13, 2005, 01:30:05; Search time 14.4262 Seconds (without alignments) 66.696 Million cell updates/sec Run on:

US-09-823-418-11 49 1 TELTRKRGLK 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apolipoprotein B-1	apolipoprotein B -		М		apolipoprotein B -	hypothetical 34.6	hypothetical prote				conserved hypothet	transcription regu	probable transcrip	hypothetical prote	isocitrate lyase (apolipoprotein B-1	apolipoprotein B -	C2-domain family p	apolipoprotein B -	apolipoprotein B -	pentose-5-phosphat	probable MADS-box	amino acid permeas	rRNA methylase - A	hypothetical prote		NADH oxidase - The	conserved hypothet
SUMMARIES	QI 1	E60950	S32802		C60950						H95070							JH0101			_						T16924	AH090	D723	G81959
	Length DB	1			269 2	274 2			309 2						219 2		550 1		1058 2					227 2						548 2
dр	Query Match		89.8	89.8	Н	81.6	-	75.5	75.5	75.5	73.5	73.5	71.4	71.4	71.4	71.4	69.4	69.4	69.4	69.4	69.4	69.4	67.3	•	67.3	•	67.3	۲.	7.	67.3
	Score	44	44	44	40	40	40	37	37	37	36	36	32	35	35	35	34	34	34	34	34	34	33	33	33	33	33	33	33	33
	Result No.	П	7	٣	4	2	w	7	89	σ	10	11	12	13	14	15	16	17	18		20			23	24	25	56		28	29

nine-cis-epoxycaro	hypothetical prote	hypothetical prote	probable regulator	myosin heavy chain	myosin-VI [similar	unconventional myo	probable membrane	ras-responsive ele	still life protein	still life protein	salivary glue prot	salivary glue prot	probable 2-oxoisov	ATP synthase delta	hypothetical prote
T04531	T05683	T26022	T35822	A44400	A54818	A59299	S59823	JC6510	T13704	T13707	S12607	833822	F69506	E84119	T19702
0	N	N	N	-	7	~	7	~	7	α	~	~	7	0	7
583	642	963	1091	1253	1254	1265	1407	1615	2044	2064	107	112	172	183	237
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67	67.3	67	67	67	67	67	67	67	67	67	65.3	65	9	65	65
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Sccession: E60950
R;Law, A.; Scott, J.
J; Lipid Res. 31, 1109-1120, 1990
A;Pitle: A cross-species comparison of the apolipoprotein B domain that binds to the LD A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Reference number: A60950
A;Molecule type: mRNA
A;Residues: 1-275 cLAM
A;Residues: 1-275 cLAM
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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Pred. No. 0.49;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
RESULT 1
E60950
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221 TSLTRKRGLK 230 1 TELTRKRGLK 10 g ò

RESULT 2

apolipoprotein B - crab-eating macaque (fragment)
C;Species Macaca fascicularis (crab-eating macaque)
C;Species Macaca fascicularis (crab-eating macaque)
C;Accession: 832802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchı Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: 832802, MUID:92075708; PMID:1742325
A;Accession: 832802
A;Status: preliminary
A;Nolecula type: mRNA
A;Residues: 1-596 < PAP>
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301
C;Superfamily: apolipoprotein B

Gaps ; 0 Query Match

89.8%; Score 44; DB 2; Length 596;
Best Local Similarity 90.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 1; Indels

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226 TRLTRKRGLK 235 1 TELTRKRGLK 10 ઠે 엄

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A;Accession: A2277

A;Accession: A2277

A;Accession: A2277

A;Accession: A2272

A;Accession: A2272

A;Accession: A2272

A;Accession: A2252

A;Accession: A2523

A;Accession: A2527

A;Accession: A2572, WIID:80705044; PMID:30448

A;Accession: A2527

A;Accession: A2527
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A; Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-5:
B; 1486-1498;1537-1555;153-1552;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968
A; Note: these fragments were derived from apod 3.0 W.; Kane, J.P.
B; Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
A; Hille: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism in A; Reference number: A28002; MUID:88106542; PMID:3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 2129-2179,2181-2235 <HA2>
A,Cross-references: GBM:M18471
A,Experimental source: intestine
A,Note: this mRNA from intestine includes a stop codon created by RNA editing in place
R,Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner,
A;Cross-references: GB:M12681; NID:g178797; PIDN:AAA51753.1; PID:g178798 R;Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Rroc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
A;Title: A partial cDNA clone for human apoliprotein B.
A;Reference number: A25774; MUID:85270450; PMID:3860836
                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A27850; A25679; A25563; A25266; A24320; A24684; A23817; A25774; A26
4452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scc
                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: DNA sequence of the human apolipoprotein B gene.
A; Reference number: A27850; MUID:8803974; PMID:3652907
A; Accession: A27850
A; Molecule type: DNA
A; Residues: 1-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'O',3433-3731,'A'; Cladares C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
BMBO J: 5,3495-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Wolecule type: mRNA

A, Residues: 1-27, N', 274-617, A', 619-1217, E', 1219-2091, V', 2093-2364, T', 2366-2679, 'Q'

A, Cross-references: GB: X04506; NID: g34330, PIDN: CAA28191.1; PID: g34331

R, Law, S.W.; Grant, S.M.; Higuchl, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr

By Coc. NBLI. Acad. Sci. U.S.A. 83, 8142-8146, 1986

A, Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino

A, Reference number: A94134; MUID: 87041416; PMID: 3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-97, 17, 99-328, VV, 330-644, II, 646-918, PV, 920-3318, DV, 3320-3426, TV, 3428-9-4132, GY, 4134-4180, EV, 4182-4563 - CHE>
A; CROSS-references: GB: J02610; NID: G178803; PIDN: AAA35549. 1; PID: G178804
A; Cross-references: GB: J02610; NID: G178803; PIDN: AAA35549. 1; PID: G178804
A; Note: a total of 236 residues were confirmed by direct sequencing of tryptic peptides R; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; Horc. Natl. Acad. Sci. U.S.A. 83, S678-5682, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein A; Accession: A24320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AjMolecule type: mRNA
A;Residues: 1-97, '1', 99-617,'A',619-941,'XXIWSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A;Residues: 1-97,'I',99-617,'A',619-941,'XXIWSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A;Cross-references: GBM4081, NLD:g18795; PIDN:AAA51752.1; PID:g553189
R;Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A;Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A;Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 485-617, A', 619-1044 <LA2>
A; Croster detences: GBM12480; NID:9178791; PIDN:AAAS1751.1; PID:9178792
A; Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; MUID:86149325; PMID:3513177
A; Molecule type: mRNA
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A; Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
A; Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
A; Molecule: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
A; Eiol. Chem. 261, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: mRNA
A Residues: 1-11,15-2539, 'S', 2541-3823,'R', 3825-4563 <CLA>
A,Residues: 1-11,15-2539, 'S', 2541-3823,'R', 3825-4563 <CLA>
A,Note: 1109-48p was also found
R,Knott, T.U.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.
R) Worleic Acids Res. 14, 7501-7503, 1986
A,Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A,Reference number: A93639; MUID:87016385; PMID:3763409
               apolipoprotein B-100 precursor – human
N;Contains: apolipoprotein B-26; apolipoprotein B-74
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81.6%;
80.0%;
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216 SRLTRKRGLK 225
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221 SSLTRKRGLK 230
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Best Local Similarity
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A,Rocession: B210, Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Omasch, M.A.; Wallis, S.C.; Biol. Chem. 261, 15364-15367, 1966
A,Title: Structure of the human apolipoprotein B gene.
A,Reference number: A92564; MUID:8705153; PMID:2946672
A,Contents: annotation; gene structure
R,Wagener, R.; Pfitzner, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
A,Title: Studies on the organization of the human apolipoprotein B 100 gene.
A,Reference number: A9015; MUID:87291140; PMID:2886136
A,Contents: annotation; gene structure
R,Weisgraber, K.H.; Rall Jfr., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A,Title: Human apolipoprotein B 100 heparin-binding sites.
A,Reference number: A9265; MUID:87280197; PMID:3308136
A,Contents: annotation; heparin binding and disulfide bond
R,Dantelli, N.; Lee, D.M.; Mok, T.
Biochem. Biophys. Res. Commun. 137, 493-499, 1986
A,Contents: annotation; calcium binding procein.
A,Reference number: A90125; WUID:8624245; PMID:3087360
A,Contents: annotation; calcium binding procein.
A,Reference number: A90125; MUID:8624265; MUID:8603600; PMID:3841204
A,Reference number: A90125; MUID:86093600; PMID:3841204
A,Reference number: A90125; MUID:86093600; PMID:3841204
A,Reference number: A90125; MUID:86093600; PMID:3841204
A,Reference number: A77180; MUID:86093600; PMID:3841204
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 2169-2179 <-HOS>
A; Residues: 2169-2179 <-HOS>
A; Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
ch encodes the 250K apoB-48, CAA encoding 2180-GIn is substituted by the stop codon TAA,
R; Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
A; Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap
A; Reference number: A55783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A35783
A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                             A; Molecule type: mRNA
A; Residues: 3056-3159 <mEH>
A; Residues: 3056-3159 <mEH>
A; Cross-treferences: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A; Cross-treferences: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
B; Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem: Biophys. Res. Commun. 148, 279-285, 11987
A; Title: Identification of a novel in-frame translational stop codon in human intestine and the communer A29659; MUID:88049670; PMID:2445342
Nucleic Acids Res. 13, 6937-6953, 1985
A;Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A;Reference number: A24269; MUID:86041888; PMID:3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 6.3;
0; Mismatches
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Best Local Similarity
Matches 9; Conserv
                                                                                                                   A; Accession: A24269
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A29659
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RESULT 4

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apolipoprotein B-100 - golden hamster (fragment)

C;Species: Mesocricetus auratus (golden hamster)

C;Species: Jabec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accesion: C60950

E;Law, A.; Scott, J.

J. Lipid Res. 31, 1109-1120, 1990

A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD A;Reference number: A60950; MUD:90324804; PMID:2373961

A;Reference number: A60950; MUD:90324804; PMID:2373961

A;Residues: 1-269 <LAW.

A;Residues: 1-269 <LAW.

A;Residues: 1-269 <LAW.

A;Residues: 1-269 <LAW.

C;Superfamily: apolipoprotein B

C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: A60550
R;Law, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A;Title: A cross species comparison of the apolipoprotein B domain that binds to the LD A;Reference number: A60950; MUD:90324804; PMID:2373961
A;Accession: A60950
A;Accession: A6095
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A; Residues: 1-779 cSNI>
A; Residues: 1-779 cSNI>
A; Residues: 1-779 cSNI>
A; Residues: 1-779 cSNI>
A; Note: this is a revision to the sequence from reference JH0101
B; Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of A; Reference number: JH0101; MUID:90236327; PMID:2332175
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
R;Smith, T.J.
Submitted to GenBank, June 1990
A;Reference number: A38864
A;Accession: JH0102
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A;Note: this sequence has been revised in reference A;8864 C;Genetics:
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Pred. No. 3;
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Pypothetical protein EC84090 [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Escherichia coli
C;Species: Bacharichia coli
C;Species: Bacharichia coli
C;Accession: B91140
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
Saawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference speciminary
A;Residues: preliminary
A;Residues: 1-309 cHAy>
A;Reperences: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:
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R. Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heit R. Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heit on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
Science 293, 498-506, 2001
A.Authors: Loftun, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A.Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A.Reference number: A95000; MUID:21357209; PMID:11463916
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CiDate: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
CiDate: 22-Oct.2011 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
CiDate: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
CiDate: 22-Oct.2001 #sequence_revision 22-Oct.2001 #text_change 09-Jul-2004
CiDate: 22-Oct.2001 #sequence_revision 2004
CiDate: 22-Oct.2001
CiDate: 22-Oct.2004
Ci
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A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SP0609 [imported] - Streptococcus pneumoniae (strain TIGR4)
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
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Pred. No. 13;
2; Mismatches 1; Indels
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Pred. No. 17;
2; Mismatches
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Best Local Similarity 70.0%;
Matches 7; Conservative 5
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70.0%;
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Best Local Similarity 70.0.
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170 TQLARQRGLK 179
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TELGKKKGLK 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P45476; GB:AE000400; GB:U00096; NID:g2367203; PIDN:AAC76243.
A;Experimental source: strain K-12, substrain MG1655
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Pred. No. 7.8;
1; Mismatches
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Pred. No. 13;
2; Mismatches 1
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Best Local Similarity 70.00
7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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642 SRLTRKRGLK 651
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170 TQLARQRGLK 179
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Length 214;

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71.4%; Score 35; DB 87.5%; Pred. No. 23;
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87.5%;
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llarity 87.5%;
Conservative (
          A; Map position: linear chromosome
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
7; Conservative
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A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUD:21429245; PMID:11544234
A; Accession: F97938
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-264 < KUR>
A; Cross-references: UNIPROT:Q8CWT1; GB:AE007317; PIDN:AAK99338.1; PID:g15458109; GSPDB:GC; Genetics:
A; Gene: glnH
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R;Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. R;Wood, D.W.; Seubal, J.C.; Ganth, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima
C;Species: In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: E72338
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Experimental source: strain C58 (Dupont)
C;Genetics
A;Gene: Au3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: E72338
A;Status: preliminary
A;Molecule type: DNA
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A;Experimental source: strain MSB8
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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A'Itlle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A'Reference number: AB2577; MUID:21608550; PMID:11743193

A'Accession: AE2934

A'Status: preliminary

A'MOlecule type: DNB

A'Residues: 1-214 «KUR»
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C;Superfamily: conserved hypothetical protein HI0670
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Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                 73.5%;
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Best Local Similarity 70.0
Matches 7; Conservative
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159 TELGKKKGLK 168
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ELLRKKGLK 119
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probable transcription regulator PA2931 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: B98348 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 231-2328, 2001 A;Reference number: A97359; MUID:21608551; PMID:11743194 Apoctechnology Agent Agrobacterium tu A;Reference number: A97359; MUID:21608551; PMID:11743194 Apoctechnology Agent Agrobacterium tu A;Reteus: preliminary A;Residues: 1-219 <*WRNDARD A;Residues: 1-210 <
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Cipecies: Arabidopsis thaliana (modesear cress)
Cipate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
Cipate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
Cipatesion: T47784
Ribhargelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
A;Reference number: 224476
A;Accession: T47784
A;Accession: T47784
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: 1112 cDAN>
A;Cross-references: UNIPROT: Q91x74; EMBL: All63527
A;Experimental source: cultivar Columbia; BAC clone F17J16
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C;Genetics:
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A;Introns: 31/3; 74/1; 103/2; 153/2; 193/2; 247/3; 309/2; 367/2; 416/1; 457/2; 517/3;
A;Note: P17J16.70
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Pred. No. 24;
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Job time : 16.4262 secs
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Q7yqq9 echinops te
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Q7yqq9 anadinia bi
Q7yqq9 zalophus ca
Q7yqq9 vulpes vulp
Q7yqq2 panthera le
Q7yqq4 manis sp. k
Q7yqq uqong dugo
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Q7yqq ochocona pr
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Q7yqn2 phalanger o
Q7yqm9 ornithorhyn
Q7yqn0 tachyglossu
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                                          January 13, 2005, 01:15:45; Search time 78.0328 Seconds (without alignments) 73.735 Million cell updates/sec
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                                                                                                                                1825181 segs, 575374646 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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07YQP0
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Q7YQQ1
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Q7YQP7
Q7TN68
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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megaderma l
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B-100 (Fragment).
Gallus gallus, (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Phalanger.
NCBI_TaxID=42473;
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MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoporein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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         07yqq9
07yqr2
07yqq8
07yqq8
07yqm7
07yqm7
07yqr4
07yqr3
07yqr3
 Q7yr12
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01-0c7-2003 (TrEMBLrel. 25, Last sequence update)
01-0c7-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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90.0%; Pred. No. 1.8;
ive 0; Mismatches
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07YQR2
07YQQ8
07YQM1
07YQM4
07YQR4
07YQQS
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TSLTRKRGLK 230
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RESULT 3 Q7YQM9

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINES-2761261, PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. Evol. 2255-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE=92075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchor G.W.;
"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Eliochim. Blophys. Acta 1086:326-334(1991).
                                                          89.8%; Score 44; DB 2; Length 405; 90.0%; Pred. No. 2.6; 1. Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.8%; Score 44; DB 2; Length 414; 90.0%; Pred. No. 2.7; 1:ive 0; Mismatches 1; Indels
                          44975 MW; 551A98557E8B081D CRC64;
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414 AA; 45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
AnnesapoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 AA
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                                                                          Local Similarity 90.0
nes 9; Conservative
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            405
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NCBI_TaxID=9541;
                                                                                                                            1 TELTRKRGLK 10
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                            405 AA;
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TISSUE=Liver;
Murray R.;
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SEQUENCE 414
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Q7YQR5;
01-OCT-2003 (
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Q28473;
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Monotremata, Ornithorhynchidae, Ornithorhynchus.
NCBI_TaxID=9258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-2761261. PubMed=12878460;

Amrine-Madeen H., Koopfil K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for euchbarian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AF548434; AAP97390.1; -.
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Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548433; AAP97389.1; --
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Tachyglossidae; Tachyglossus.
NCBI_TaxID=9261;
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                                                                                                     Score 44; DB 2; Length 387;
Pred, No. 2.5;
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387 387
387 AA; 43230 MW; 8300A9D7C54B42B0 CRC64;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.6;
0; Mismatches
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EMBL; AF548431; AAP97387.1;
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                 Lipoprotein.
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01-OCT-2003
01-OCT-2003
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Q7YQN0

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Gaps

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'Complete cDNA and derived protein sequence of human apolipoprotein
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                                          Nucleic Acids Res. 14:7501-7503(1986)
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P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Last sequence update)
05-JUL_2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
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Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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90.0%; Pred. No. 24;
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  to the EMBL/GenBank/DDBJ databases.
                                                                                                                  66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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EMBL; M15421; AAAS1758.1; -.

PIR; A27850; LBHUBA
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005519; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport; NAS.
                                                                                                                                                      Score 44; DB 2;
Pred. No. 4;
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                                                                                                                                                      89.8%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Submitted (FEB-1992) to th
EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                              9; Conservative
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596
596 AA;
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                                                            Lipoprotein.
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APB_HUMAN
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SEQUENCE OF 1-291 FROM N.A.

MEDILINE=86149325; PubMed=3513177;

MEDILINE=86149325; PubMed=3513177;

Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;

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MEDLINE-85330628; PubMed=2994225;
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Science 230:37-43(1985). Ь SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE-86041888; PubMed=3903660;
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characterization of mRNA."; SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
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MEDLINE=8704116; PubMed=3464946;
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WEDLINE=95190020; PubMed=7883971;
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                                                                                                                    MEDIINE-88018019; PubMed=365919;
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MEDLINE=89098975; PubMed=2563166;
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VARIANT FDB CYS-3558.
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Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mandel C.M., Frost P.H., Malloy M.J., Schumaker V.M., Kane J.D.; "Familial ligand-defective apolipoprotein B. Identification of a ne mutation that decreases LDL receptor binding affinity.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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GO, GO:0005319; F:lipid transporter activity; IEA.
GO, GO:0005819; F:lipid transporter activity; IEA.
InterPro: IPR009454; DUF1081.
InterPro: IPR001747; Lipid_transport_N.
PEGM: PF06448; DUF1081; 1.
Pfam: PF06448; UVITCH109enin_N; 1.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
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                                                                                                                   Clin. Invest. 95:1225-1234(1995).
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                                                                                                                                                                                                                      MEDLINE=97044521; PubMed=8889592;
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Hum. Mutat. 10:160-163(1997).
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es 9, Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 35;
0; Mismatches 1; Indels
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Pred. No. 4.2;
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                                4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032144; AAH32144.1; -.
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Last annotation update)
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80.0%;
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SMART; SM00638; LPD_N; 1.
                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                               ACSL3 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednences.
                                                                                                                                                             3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                              1 TELTRKRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA
                 Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung;
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                                                                                                                                                                                                                                                                                                                                                Name=ACSL3;
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                                                                                                                                                                                                                                                            Q6PIM8;
                                                                                                                                                                                                                                           Q6PIM8
                                                                                                                                                                                                         RESULT 10
Q6PIM8
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AAH32144
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TISSUB-LUNG;

WEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MAISTOR R.L., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabak S.A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodiguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T Generation and initial analysis of more than 15,000 full-length human
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MEDLINE=97321062; PubMed=9177793;
Minekura H., Fujino T., Kang M.-J., Fujita T., Endo Y., Yamamoto T.T.;
Minekura dyl-coenzyme A synthetase 3 cDNA and localization of its gene (ACS3) to chromosome band 2q34-q35.";
Genomics 42:180-181(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description Standard, FRI; '20 An. 095573; 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 05-0UJ-2004 (Rel. 44, Last annotation update) Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) (Long-chain acyl-CoA syntherase 3) (LACS 3). Name-ACSL3; Synonyma-FACL3, ACS3, LACS3; Homo sapiens (Human).
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                                                                                                                                                                                LONGO SUPERIOR (METAZORA).
BUNARODES, METAZORA: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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80.0%; Pred. No. 4.2;
.ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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03-MAR-2004 (TrEMBLrel. 27, Last sequence update) 03-MAR-2004 (TrEMBLrel. 27, Last annotation update) ACSL3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                            Homo sapiens (Human)
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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AB061434; BAB72139.1; JOINED.
AB061435; BAB72139.1; JOINED.
NCE 720 AA; 80345 MW; 845959A765BC6BF6 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last seq
02-MAR-2004 (TrEMBLrel. 27, Last ann
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SEQUENCE 720 AA; 80419 MW; AJ
                                                                                                                                                                                                                                                                                                                   cDNA sequences.
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Les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                                      and mouse
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SEQUENCE
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         REPARA REPAREMENT OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                            MEDLINE=21564184; PubMed=11707336; DOI=10.1016/S0378-1119(01)00714-4; Minekura H., Kang M.-J., Inagaki Y., Suzuki H., Sato H., Fujino T., Yamamoto T.T.; "Genomic organization and transcription units of the human acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pancreas;
MEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz F.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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PROSITE; PS00455; AMP BINDING; 1.
Fatty acid metabolism; Ligame; Magnesium; Multigene family.
SEQUENCE 720 AA; 80345 MW; 845959A765BC6BF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 41; DB 1; Length 720; 80.0%; Pred. No. 20; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 602371; -.
GO; GO:0004321; F:fatty-acyl-CoA synthase activity; TAS.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     720 AA.
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EMBL, AB061712; BAB72074.1; -.
Genew, HGNC:3570; ACSL3.
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M. A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Gene 278:185-192(2001).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R., Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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80.0%; Pred. No. 20;
iive 1; Mismatches 1; Indels
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR000873; AMP-bind.
PRUNTS; PR05014; AMPBINDING.
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O'TCOT-2003 (TrEMBLrel. 25, Last sequence update)

O'TCOT-2003 (TrEMBLrel. 25, Last sequence update)

O'TCOT-2003 (TrEMBLrel. 25, Last annotation update)

NAME=apol-100;

NAME=apol-100;

NAME=apol-100;

NAME=apol-100;

NCBI TaxID=9813;

NCBI TaxID
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Query Match

83.7%; Score 41; DB 2; Length 720;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 1; Indels
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80.0%; Pred. No. 11;
tive 1; Mismatches 1; Indels
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263 263
263 AA; 29532 MW; 536CF6149C1D062A CRC64;
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Best Local Similarity 80.0
Matches 8; Conservative
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633 TELARKKGLK 642
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07.YQQ0;
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Search completed: January 13, 2005, 01:51:02 Job time : 78.0328 secs

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January 13, 2005, 01:14:40; Search time 77.2131 Seconds (without alignments) 46.460 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                       OM protein - protein search, using sw model
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50
1 TDLTRKRGLK 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:*
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	Description	Aay30693 Apo-B100			Ω		Aaw96892 ApoB-100	Abj37575 Heparin b		Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo		Adj57400 Human apo	-	Apolin	Aaw96826 Amino aci	Aau98981 Human apo	Add48677 Human Pro	Aao15893 Human apo	Abr40253 Human ali
SUMMARIES	Ü	AAY30693	AAY30692	AAW57205	AAWS7207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981	ADD48677	AA015893	ABR40253
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٠	Query Match	100.0	92.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0
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BESULT 1 AAY30693 X AAY30693; X T 17-NOV-1999 (first entry) X X T model00 derived peptide showing a proteoglycan receptor n X X X X X X X X X X X X X X X X X X X

ALIGNMENTS

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WO9946598-A1. 16-SEP-1999.

98US-0077618P. 99WO-US004805. 05-MAR-1999; 10-MAR-1998;

(REGC) UNIV CALIFORNIA.

Innerarity TL, Boren JOS; WPI; 1999-551509/46.

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

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Sequence 10 AA;

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receptor mutations. They were created to identify compounds which modulate atheroaclerosis. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the connection of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                     Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
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Score 46; DB 2; Length 10;
Pred. No. 0.038;
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Pred. No. 0.25;
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92.0%;
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TRLTRKRGLK 11
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KABTKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                    Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                             Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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                                                                                                B 100 binding site peptide analogue peptide B.
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Pred. No. 0.3;
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                          AAW57207 standard; peptide; 13 AA.
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90.0%;
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Modified-site
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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apob-100). ILYAQ-XI-KAKARRHS-X2-T-Z2 (I) XI = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent captactic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to which is active as such or as part of a 98-as apptide, inhibits of the prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of the residues Se defort thromboplastin and of platelets by thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                               Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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90.0%; Pred. No. 0.34;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW96892 standard; peptide; 15 AA.
Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96GB-00009702
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                                                                                                                                                                             prothrombinase complex.
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Best Local Similarity
9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                 WO9743311-A1
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                                                                                                                                                                                                                                          Synthetic
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which comprises a peptide having at least one sulphated or sulphonated charged and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                             The invention relates to a novel ligand for binding a target biomolecule,
                                                                                                                                                                 Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "attached to retinoic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
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Pred. No. 0.46;
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                                                                                            Maynard
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                                                                                                                                                                                                                                          Disclosure; Fig 2; 79pp; English.
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 20-JUL-2001; 2001US-0306726P
                                                                                          Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-GB002610
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TDLTRKRGLK 10
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                                                                                                                            WPI; 2003-300420/29
                                    (ETHZ-) ETH ZUERICH (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human apolipoprotein B-100 (app8-100). Apo8-100 is a major approtein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96878-97 represent nuclear localisation signal sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                   Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE
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98US-00079030.
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90.0%;
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                                                                                                                                                                                                                                                                                                                   Hoogeveen RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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9; Conserv
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                                                                                                             WO9856938-A1
                                                                                                                                                                                    10-JUN-1998;
                                                                                                                                                                                                                         13-JUN-1997;
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                                                                                                                                                  17-DEC-1998
                                                                                                                                                                                                                                                                                                                   Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                               treatment.
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKNKHR (1) or TTRLTRKRGLK (2), or their clamers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
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Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57209 standard; peptide; 22
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90.0%;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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8 g The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

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particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL. In a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                     Score 42; DB 2; Length 22;
Pred. No. 0.5;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14541 standard; peptide; 34 AA.
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                                                                                                                                                                                                                                                                                   84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2001; 2001WO-GB003212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ARKT-) ARK THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                   1 TDLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                   7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-17977/23.
                                                                                                                                                                                                                                                    Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE14541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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Query Match

à 셤 AAW96876

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(associated with hypercysteinaemia and venous thrombosis) and factor VII mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is particularly suited to routine screening. It also allows mutant protein in a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method too detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vaint thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apoE indicates increased risk of developing Alzheimer's disease), thermostable 5,10-methylenetetrahydrofolate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                                                                                                                                                                       Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%; Score 42; DB 2 90.0%; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schenk V;
                                                                                                                                                                                                                                                  Human apolipoprotein peptide fragment #1.
                                                                                                               AAW64587 standard; peptide; 37 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·98EP-00890007.
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                                                                                                                                                                                                        (first entry)
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  11 TRLTRKRGLK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TDLTRKRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-416142/36.
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1998;
                                                                                                                                                                                                        23-OCT-1998
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                                                                                                                                                            AAW64587;
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AAW96845
ID AAW96
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                                                                                          AAW64587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollpoprotein; Diding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes, arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                             Length 34;
                                                                                                                                                            1; Indels
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                                                                                                             Score 42; DB 5;
Pred. No. 0.78;
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Pred. No. 0.82;
0; Mismatches
                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                             AAW96876 Btandard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Fig 12C; 293pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00874807.
98US-00079030.
                                                                                                             84.0%;
90.0%;
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ilarity 90.0%;
Conservative
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                                                                                                                                                            9; Conservative
                                                                                                                                                                                                      1 TDLTRKRGLK 10
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                                                                                                                                    Local Similarity
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Best Local Similarity
Matches 9; Conserv
                                                                   Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
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2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TDLTRKRGLK 10
                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide,
                                                                                                                                                                                                WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                         Sequence 343 AA;
  WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                      30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                  04-FEB-2000;
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                       09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG52504;
                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                             AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                         Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoms; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                   to LDL or VLDL lipoprotein - for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #5193 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2; Length 51;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                   bound
                                                    Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                         Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                   Composition comprising nucleic acid used for delivering nucleic acid to
                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB37687 standard; peptide; 343 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrosis and arteriosclerosis
                                                                                                                                                                                                                             98US-00079030.
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90.0%;
                                                                                                                                                                                               98WO-US011927,
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                                22-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDLTRKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                             WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51 AA;
                                                                                                                                Homo sapiens
                                                                                                                                                     WO9856938-A1
                                                                                                                                                                                               .0-JUN-1998;
                                                                                                                                                                                                                    13-JUN-1997;
                                                                                                                                                                                                                               14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2002
                                                                                                                                                                           17-DEC-1998
                                                                                                                                                                                                                                                                                                                                         treatment.
           AAW96845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB37687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fatches
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID No 31152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG52504 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                         ; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
30-JAN-2001; 2001WO-US000669
                                                              2000US-0180312P
                                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312P
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(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK,

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements / fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipideamia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the printed specification ftp.wipo.int/pub/published_pct_sequence

Sequence 343 AA;

Gaps 0 84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 7.8; ive 0; Mismatches 1; Indels Query Match Best Local Similarity 90.09

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1 TDLTRKRGLK 10

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| ||||||| 169 TRLTRKRGLK 178

Search completed: January 13, 2005, 01:43:02 Job time : 78.3798 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 13, 2005, 01:30:05; Search time 14.4262 Seconds (without alignments) 66.696 Million cell updates/sec Run on:

US-09-823-418-12 50 1 TDLTRKRGLK 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB ID Result No.

			i	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
44	88.0	275	~	E60950	apolipoprotein B-1
42	84.0	296	~	S32802	apolipoprotein B -
42	84.0	4563	Н	LPHUB	apolipoprotein B-1
40	80.0	274	N	A60950	apolipoprotein B-1
39		269	N	C60950	apolipoprotein B-1
39		779	N	JH0102	apolipoprotein B .
37	74.0	1091	~	T35822	probable regulato
36	72.0	266	N	S60674	hypothetical prote
35	70.0	187	N	T21671	hypothetical prote
32	70.0	309	H	E65112	hypothetical 34.6
32	70.0	309	~	E85985	-4
35	70.0	309	N	B91140	_
35	70.0	382	-	A44056	ņ
35	70.0	1217	~	T25894	_
35	70.0	3450	7	T26963	ᄓ
35	70.0	3461	N	T26964	_
34	68.0	168	N	T03168	_
34	68.0	206	~	T01788	aminoglycoside 6'-
34	68.0	211	7	F75474	hypothetical prote
34	68.0	493	N	E71008	hypothetical prote
34	68.0	680	~	S29682	
	68.0	684	~	S29683	DNA gyrase B, novo
34	68.0	989	~	T10969	DNA topoisomerase
34	68.0	05	~	865460	apolipoprotein B
34		1253	Н	₹*	myosin heavy chain
34	68.0	1254	~	54	myosin-VI [similar
34	68.0	56	~	A59299	unconventional my
34	68.0	1615	0	651	ras-responsive ele
34	68.0	77	N	JT0382	apolipoprotein B -

apolipoprotein B -	hypothetical prote	hypothetical prote	hypothetical prote	probable transcrip	ubiquinol-cytochro	replication protei	probable membrane	apolipoprotein B-1	probable polyketid	hypothetical prote	conserved hypothet	transcription regu	probable transcrip	conserved hypothet	pantoate-beta-alan
146569	D75018	H95070	F97938	B72475	862596	S60672	S55980	JH0101	T03223	B64497	E72338	AE2934	B98348	AE0876	F82832
7	0	~	7	N	~	~	7	7	7	7	7	7	7	~	~
2629	102	254	264	325	339	391	402	784	2100	70	149	214	219	252	281
68.0	0.99	0.99	0.99	0.99	0.99	0.99	0.99	66.0	66.0	64.0	64.0	64.0	64.0	64.0	64.0
				33 66.0											

ALIGNMENTS

apolipoprotein B-100 - chicken (fragment)

C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Jubec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: E60950
B;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the Lipid Reservance number: A60950; MUD:90324804; PMID:2373961
A;Reference number: A60950; MUD:90324804; PMID:2373961
A;Reference number: A60950; MUD:900204804; PMID:2373961
A;Residues: 1-275 <LAW.
A;Residues: 1-275 <LAW.
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein ö Gaps .. 0 Query Match

88.0%; Score 44; DB 2; Length 275;
Best Local Similarity 90.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 1; Indels RESULT 1

221 TSLTRKRGLK 230 1 TDLTRKRGLK 10 g ઠે

RESULT 2

politoprotein B - crab-eating macaque (fragment)

Cispecies: Macaca fascicularis (crab-eating macaque)

Cispecies: Macaca fascicularis (crab-eating macaque)

Cispecies: Objective: Ocidan-1995 #sequence_revision Ocidan-1995 #text_change Og-Jul-2004

Cispace, M.B.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchn Biochim. Biochim

ö Query Match

84.0%; Score 42; DB 2; Length 596;
Best Local Similarity 90.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 1; Indels

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Gaps

226 TRLTRKRGLK 235 1 TDLTRKRGLK 10 쉱 ò

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Aprile 1282-2721,2742-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180, Aprile type: mRNA
A, Residues: 1282-2721,2742-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180, Aprile streferences: G8 M15421, NID:9178817, PID:9178818
R, Hardman, D.A.; Protter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yaman, Biochemistry 26, 5478-5486, 1987
Affile: Structural comparison of human apolipoproteins B-48 and B-100.
A; Reference number: A29671; MUID:88050832; PMID:3676265
A; Accession: A29671
A; Molecule type: mRNA
A; Residues: 1671-2323, PWW, 2327-2352,'H',2354-2398 (HAR>
A; Residues: 1671-2323, PWW, 2327-2352,'H',2354-2398 (HAR>
A; Residues: 1671-2323, PWW, 2327-2352,'H', 2354-2398 (HAR>
A; Residues: 1671-2323, PWW, 2377-239, 1985
A; R; Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.
Atherosclerosis 58, 277-289, 1985
A; Title: Molecular cloning of human LDL apolipoprotein B cDNA, Evidence for more than on A; Reference number: A90084; MUID:86130855; PMID:3841481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: A2572

A, Molecule type: mRNA

A, Residues: 4219-4337, S., 4339-4563 < PFI>

A, Molecule type: mRNA

A, Fesidues: 4219-4337, S., 4339-4563 < PFI>

A, Cross-references: GB M36676

B; Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.

Broc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985

A, Reference number: A24738; MUID:86042646; PMID:2932736

A, Accession: A24738

A, Accession: A24738

A, Molecule type: mRNA

A, Residues: 'N' 3729-3731''', 3333-3875, 'A', 3877-3948''F', 3950-3963, 'Y', 3965-3982,'S', 3'

A, Cross-references: GB: M12413; NID:g178735; PIDN:AAA51742.1; PID:g178736

B, Chen, S.H.; Habib, G, Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Ca

A, Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in A, Reference number: A40133; MUID:88018019; PMID:3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 51-75;101-110,129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-5
A; Residues: 51-75;101-110,129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-5
A; 1486-1498;1537-1556;1553-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968
A; Note: these fragments were derived from apo48
B; Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
Biochem. Biophys Res. Commun. 149, 1214-1219, 1987
A; Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism A; Reference number: A28002; MUID:88106542; PMID:3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a human apolipoprotein B 100-spe
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A,Residues: 2129-2179,2181-2235 <HA2>
A,Residues: 2129-2179,1818471
A,Cross-references: GB:M18471
A,Experimental source: intestine
A,Note: this mRNA from intestine includes a stop codon created by RNA editing in place
R,Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner,
                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A,Residues: 709-791, SSSWKAASHGCPHSAGD',810-906 <DEE>
A;Residues: 709-791, SSSWKAASHGCPHSAGD',810-906 <DEE>
A;Cross-references: GB:K03175; NID:g178821, PIDN:AAAS1759.1; PID:g178822
B;Cross-references: GB:K03175; NID:g178821, G.; Bjursell, G.
Gene 49, 29-51, 1986
A;Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74
A;Title: Analysis of the human apolipoproteip B gene; complete structure of the B-74
A;Reference number: A91565; MUID:87191999; PMID:2883086
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A,Cross-references: GB:M12681; NID:g178797; PIDN:AAA51753.1; PID:g178798 R;Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Rroce. Natl. Acad. Sci. US.A. 82, 4983-4986, 1985
A;Title: A partial cDNA clone for human apoliprotein B.
A;Reference number: A25774; MUID:85270450; PMID:3860836
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A,Molecule type: mRNA
A,Residues: 3846-4298 <SHO>
R,Fitzner, R., Magner, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A,Title: Isolation, expression and characterization of a A,Reference number: A25572; MUID:87076044; PMID:3024665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 2165-2179 <CH1>
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A; Residues: 1-617,'A', 619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'
A; Residues: 1-617,'A', 619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'
A; Cross-references: UNIPROT:P04114; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIF
R; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A; Reference number: A91058; MUID:87161758; PMID:3030729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-617, A, 619-703, P', 705-792, R', 794-1270, S', 1272-1866, G', 1868-2036, N', 2 4189-4220, M', 4222-4563 cLAW>
A70ce: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and Ts. Chem. S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M. J. Biol. Chem. 261, 12918-12921, 1986
A;Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A;Reference number: A92556; MUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ajmolecule type: mRNA
A;Residues: 485-617, 'A',618-1044 <LA2>
A;Residues: 485-617, 'A',618-1044 <LA2>
A;Cross-references: Gsm12480; NID:g178791; PIDN:AAAS1751.1; PID:g178792
R;Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki Prot. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A;Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr A;Reference number: A94088; MUID:86149325; PMID:3513177
                                                                                              N'Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A264452; IG1909; IS9S10; IS9S10; IS9469; I84664; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sco
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R; Law, S.W.; Grant, S.W.; Higuchi, R.; Hospatrankar, A.; Lackner, K.; Lee, N.; Brewer Jr Proc. Natl. Acad. Sci. U.S.A. 83, 814.2-8146, 1996
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino A; Reference number: A94134; MUID:87041416; PMID:3464946
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A; Residues: 1-97, 1: 99-328, VV, 330-644, I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
9-4132, 'G', 4134-4180, 'E', 4182-4563 < CHE>
A; Cross-references: GB. J02610; MID: 9178803; PIDN: AAA35549.1; PID: 9178804

A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
A; Note: A total of 236 residues were confirmed by direct sequencing of tryptic peptides
B; Note: A total of 236 residues were confirmed by direct sequencing of tryptic peptides
B; Note: A saturation of the confirmed by direct sequencing of tryptic peptides
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A; Reference number: A24320; MUID: 86287319; PMID: 3461454
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A; Residues: 1-11.15-2539, 'S', 2541-3823,'R', 3825-4563 <CLA>
A; Note: 1109-Agg was also found
R; Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.
Nuclaic, Asids Res. 14, 7561-7503, 1986
A; Title: Complete CDNA, and derived protein sequence of human apolipoprotein B-100.
A; Reference number: A93639; MUID:87016385; PMID:3763409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Accession: A27850
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A; Molecule type: mRNA
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Gaps

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apolipoprotein B-100 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A60950
R;Law, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A;Title: A cross species comparison of the apolipoprotein B domain that binds to the LI
A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: A60950
A;Accession: A60950
A;Accession: A60950
A;Cross-references: UNIPROT:Q7M2U9
A;Cross-references:UNIPROT:Q7M2U9
A;Cr
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C'Species: Mesocricetus auratus (golden hamster)
C'Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C'Accession: C60950
B'Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A'Altile: A cross-species comparison of the apolipoprotein B domain that binds to the Li A'Reference number: A60950; MUID:90324804; PMID:2373961
A'Reference number: A60950, MUID:90324804; PMID:2373961
A'Residues: 1-269 cLAM
A'Residues: 1-269 cLAM
A'Residues: 1-269 cLAM
A'Residues: 1-269 cLAM
A'Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C'Superfamily: apolipoprotein B
C'Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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C; Species: Mesocricetus auratus (golden hamster)
C; Species: Mesocricetus auratus (golden hamster)
C; Date: 11-Apr.1993 #sequence_revision 17-Apr.1993 #text_change 09-Jul-2004
C; Accession: JH0102
R; Smith, T.J.
submitted to GenBank, June 1990
A; Mclecule type: DNA
A; Mcsession: JH0102
A; Molecule type: DNA
A; Mcseiduses: 1-779 < cSMI>
A; Museiduse: 1-779 < cSMI>
A; Museiduse: 1-779 < cSMI>
A; Museiduse: 1-779 < cSMI>
A; Muteicule this is a revision to the sequence from reference JH0101
R; Matther D; J109 
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of A; Contents: annotation
A; Note: this sequence has been revised in reference A38864
C; Genetics:
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Pred. No. 2.9;
1; Mismatches
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221 SSLTRKRGLK 230
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By Blackhart, B.D; Ludwig, E.M; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;

J. Biol. Chem. 261, 15364-15367, 1986

AyTitle: Structure of the human apolipoprotein B gene.

Aymoner: annotation; gene structure

By Biol. Chem. Hoppe-Seyler 368, 419-425, 1987

AyTitle: Studies on the organization of the human apolipoprotein B 100 gene.

Aymonent: annotation; gene structure

Aymolecule type: Aymolecule By Biol.

Aymolecule: Apolis; Wuld. 1987

Aymolecule: annotation; gene structure

By Weisgraber, K.H.; Rall Jr., S.C.

J. Biol. Chem. 262, 11097-11103, 1987

Aymolecule: annotation; protein B-100 heparin-binding sites.

Aymolecule: annotation; heparin binding and disulfide bond

Aymolecule: Apolipoprotein B is a calcium binding protein.

Aymolecule: annotation; calcium binding protein.

Aymolecule: annotation; calcium binding protein.

Aymolecule: Apolipoprotein B is a calcium binding protein.

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A; Residues: 2169-2179 <hOspin the sequence shown to the sequence shown the sequence shown to the sequence shown to the sequence shown the sequence the 250K apo8-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, Ry Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Ry Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Contentes disulfide bonds
A; Contentes disulfide bonds
A; Molecule type: protein
A; Residues: 28-41;76-97,11,99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5-215-249;259-249;259-266;357-399;455-490;512-5-215-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259-249;259
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A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUD:84208786; PMID:6373369
A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-892, K',894-896 <LEI>
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A; Residues: 3056-3159 <MEH>
A; Residues: 3056-3159 <MEH>
A; Residues: 3056-3159 <MEH>
A; Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A; Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; BID:g929609
B; Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in human intestine
A; Reference number: A29659; MUID:88049670; PMID:2445342
Nucleic Acids Res. 13, 6937-6953, 1985
A;Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A;Reference number: A24269; MUID:86041888; PMID:3903660
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Pred. No. 16;
0; Mismatches 1; Indels
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Matches 9; Conser
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hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (etrain :
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R, Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher Iller, L.i.; Grotheck, E.j.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUD:21074935; PMID:11206551

A; Accession: E85985

A; Status: preliminary
A; Molecule type: DNA
A; Cosserences: UNIPROT: P45476; GB: ABC005174; NID: 912517832; PIDN: AAG58345.1; GSPDB:
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A;Cross-references: UNIPROT:P45476; GB:AE000400; GB:U00096; NID:g2367203; PIDN:AAC76243
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Escherichia coil (strain C; Date: 10-Sep-1999 #text_change 09-Jul-2004 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C; Accession: E65112 Baturer, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617; PMID:9278503
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A;Gene: yhoc
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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Pred. No. 32;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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70.0%; Pred. No. 20;
iive 1; Mismatches
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Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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54 TDLPKKRGKK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable regulatory protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accesion: T3582
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B;Murphy, L.; Harris, Data Library, February 1999
A;Reference number: Z21589
A;Accession: T3582
A;Accession
                                  C;Superfamily: apolipoprotein B
K;Reywords: athersoslersosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
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C;Species: Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Accession: S66674
R;Nesvera, J.; Patek, M.; Hochmannova, J.; Abrhamova, Z.
Biubmitted to the EMBL Data Library, August 1995
A;Description: Complete nucleotide sequence of the cryptic plasmid pGA1 from Corynebacte
A;Reference number: S66673
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A, Molecule type: DNA
A, Fosidues: 1-266 <NES>
A, Cross-references: UNIPROT: Q46059; EMBL: X90817; NID: 9951006; PIDN: CAA62329.1; PID: 99510
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                                                                                                                                                                                                      DB 2;
12;
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                                                                                                                                                                                                  78.0%; Score 39; DB 100.0%; Pred. No. 12; ative 0; Mismatches
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87.5%;
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Best Local Similarity 100.0
Matches 8; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6, Conservative
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211 DLSRKKGIK 219
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|DLTRRRGL 736
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A;Introns: 270/3; 757/2; 1105/1; 1259/3; 2312/2; 2613/1; 2825/2; 3180/1; 3217/3; 3257/3
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R; Harris, B.

R; Redeence number: 220292

A; Residues: 1-3450 < WIL>

A; Residues: 1-3450 < WIL>

A; Residues: 220408

R; Harris, B.

R; Harris
                                                                  hypothetical protein T19B4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28994
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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A;Map position: 1
A;Introns: 66/1; 119/3; 321/3; 552/3; 1123/2; 1197/2
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Job time : 15.4262 secs
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Best Local Similarity 100.
Matches 7; Conservative
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2762 DVTRKRGI 2769
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290 TDLTRKR 296
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Best Local S
Matches 6
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C;Species: canine coronavirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A4056
R;Vennema, H.; Rossen, J.W.A.; Wesseling, J.; Horzinek, M.C.; Rottier, P.J.M.
Virology 191, 134-140, 1992
A;Title: Genomic organization and expression of the 3' end of the canine and feline ente A;Recession: A44056; MUID:93033103; PMID:1329312
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Residues: 1-382 <VEN>
A;Cross-references: UNIPROT:Q04700; GB:X66717; NID:958849; PIDN:CAA47246.1; PID:958850
C;Genetics:
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C,Superfamily: coronavirus nucleocapsid protein
C,Keywords: glycoprotein; nucleocapsid
F;28,134,154,172,364/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Gene: yhcC
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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A;Gene: EC64090
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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Pred. No. 32;
1; Mismatches 2; Indels
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Pred. No. 39;
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Pred. No. 32;
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Similarity 75.0%;
6; Conservative ;
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Phalanger orientalis (gray cuscus).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Phalanger.
NCBI_TaxID=42473;
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MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; PubMed=12878460;
Marine-Madaen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                               Apolipoprotein B-100 (Fragment).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein B 100 (Fragment).
Name=apoB-100;
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NCBI_TaxID=9031;
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                                                January 13, 2005, 01:15:45; Search time 78.0328 Seconds (without alignments) 73.735 Million cell updates/sec
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Q7ygr3
     GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                   1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
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Q7YQR5
Q28473
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Q13788
APB HUMAN
                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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seq length: 200000000
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Q7yr07
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Last annotation update)
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Aotus vociferis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

BELLINE-2761261, PubMed=12878460;

Amrine-Madesn H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic merker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 2255-240(2003).

EMBL; AFS48396; AAP97352.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Marotti K.R., Malchior G.W.,
"Apo B metabolism in the cynomolgus monkey: evidence for post-
transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%; Score 42; DB 2; Length 414; 90.0%; Pred. No. 7;
                                                                                         Indels
                     44975 MW; 551A98557E8B081D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Apolipoprotein B (Fragment).
                                                   88.0%; Score 44; DB 2
90.0%; Pred. No. 2.7;
tive 0; Mismatches
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NCBI TaxID=9541;
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SEQUENCE 414
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Monotremata, Ornithorhynchidae, Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; An ewe phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Mylogenetic marker, apolitoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tachygloseus aculeatus (Australian echidna).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Monotremata, Tachyglossidae, Tachyglossus.
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387 387
387 AA; 43230 MW; 8300A9D7C54B42B0 CRC64;
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400 AA; 44611 MW; DC79873CA6D01CFA CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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Pred. No. 2.6;
0; Mismatches 1
                                                                                                  Score 44; DB 2;
Pred. No. 2.5;
0; Mismatches
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90.0%;
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EMBL; AF548431; AAP97387.1;
                                                                                                                                    9; Conservative
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Best Local Similarity
Matches 9; Conserv
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NON TER
NON TER
SEQUENCE 40
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01-OCT-2003 (
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N TER
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"Complete cDNA and derived protein sequence of human apolipoprotein
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Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                           Biol. Chem. 261:12918-12921(1986)
                                                                                                                                                                                                                                                 derived amino acid sequence.";
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                                                                                          DNA 6:363-372(1987).
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P04114; O00502; Q13787;
01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein
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MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
                                                                                                                                                                                                                                                                                                                                                        gene; complete structure of
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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596 596
596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
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MEDLINE=87191999; PubMed=2883086;
Carlbson P., Darnfors C., Olofsson S.O., Bjursell G.;
Carlbson P., Darnfors C., Olofsson S.O., Ejursell G.;
"Analysis of human apolipoprotein B gene; complete the B-74 region.";
Gene 49:20-51(1986).
                                                                                                                                                                                                                            01, Last sequence upuace, 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:000689; F:lipid transport; NAS.
NON TER
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Pred. No. 10;
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Pred. No. 63;
0; Mismatches
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PIR; A27850; LPHUB.
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        EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                        Local Similarity 90.0 tes 9; Conservative
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                             Lipoprotein.
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Evoy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,

Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,

Mahley R.W., Scott J.;

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of gene expression, and chromosomal localization."; MEDLINE=86149325; PubMed=3513177; Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V., Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.; "Isolation of a cDNA clone encoding the amino-terminal region of human Ь SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.,
"The complete cDNA and amino acid sequence of human apolipoprotein Bn D.F., Lusis A.J.; SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181 MEDLINE=86093680; PubMed=3841204; SEQUENCE FROM N.A.
MEDLINE-87041416; PubMed=3464946;
MEDLINE-87041416; PubMed=3464946;
Leaw S.W., Grant Z.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
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MEDLINE=95190020; PubMed=7883971;
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                                                                                                                            PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDLINE-88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cal S.-J., Deelypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.;
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Science 238:363-366(1987).
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Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,

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Complete protein s.gequence and identification of structural domains

Nature 323:734-738(1986).
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          SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
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Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT LEU-2739.
MEDLINE=91016974; PubMed=2216805;
Huang L.-S., Gavish D., Breslow J.L.;
Hosquence polymorphism in the human apoB gene at position 8344.";
Nucleic Acids Res. 18:5922-5922(1990).
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"Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene.";
Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITOYLATION OF CYS-1112.
MEDLINE-20141590; PubMed=10679026;
Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and triglycerides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89098975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86242245; Pubmed=3087360; Dashti N., Lee D.M., Mok T.; "Apolipoprotein B is a calcium binding protein."; Biochem. Biophys. Res. Commun. 137:493-499(1986).
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MEDLINE=91071750; PubMed=1979313;
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VARIANT FDB CYS-3558.

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MEDLINE=97403938; PubMed=9259199;
Rabes 'D.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krempf M., Giraudet P., Junion C.,
Emplial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hum. Genet. 102:44-49(1998).
-1- FUNCTION: Apolipoprotein B is a major protein constituent of
chlomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Ap
B-100 functions as a recognition signal for the cellular binding
and internalization of LDL particles by the apoB/E receptor.
-1- SUBCELLULAR LOCATION: Secreted.
                                                           new
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         Love J.A.,
ine J.P.;
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Polrier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arvaeler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene
PCR-SSCP.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P. Familial ligand-defective apolipoprotein B. Identification of mutation that decreases LDL receptor binding affinity.", J. Clin. Invest. 95:1225-1234 (1995).
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Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7324608; AAP72970.1;
GO; GO:000519; F:lipid transporter activity; IEA.
GO; GO:0005869; P:lipid transport; IEA.
InterPro; IPR009454; DUF1081.
InterPro; IPR000745; Lipid_transport.
Pfam; PF01347; Vitellogenin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98141125; PubMed=9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene or
hypocholesterolemia.";
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
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Pred. No. 91;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           population."
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Echinops telfáiri (Lesser hedgehog tenrec).
Wararyota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.
NCBI_TaxID=9371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ictonyx striatus (striped polecat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AF548412; AAP97368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Mylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 40; DB 2; Length 304;
80.0%; Pred. No. 13;
ive 1; Mismatches 1; Indels
                             Indels
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304 AA; 34264 MW; 468F4409260D6358 CRC64;
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                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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                           1; Mismatches
     Pred. No. 12;
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  80.08;
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                           8; Conservative
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Matches 8; Conservative
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221 SSLTRKRGLK 230
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                                                                           1 TDLTRKRGLK
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314 AA;
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ictonyx.
NCBI_TaxID=55050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=apoB-100;
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NON TER
31
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01-OCT-2003
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SEQUENCE
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                                                                                                                                                                                                             RESULT 12
Q7YQP9
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                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Mylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Procavia capensis (Cape hyrax) (Rock dassie).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B-100 (Fragment).
Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                    Score 42; DB 2; Length 4563;
Pred. No. 91;
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                                                4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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274 AA; 30505 MW; CALEIBE360AAB8F2 CRC64;
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Last annotation update)
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80.0%; Pred. No. 11;
tive 1; Mismatches
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MEDLINE=90324804; PubMed=2373961;
Law A., Scott J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Cree 01-OCT-2003 (TrEMBLrel. 25, Last 01-OCT-2003 (TrEMBLrel. 25, Last Apolipoprotein B 100 (Fragment).
                                                                                                    84.0%;
90.0%;
SMART; SM00638; LPD_N; 1.
                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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206 SSLTRKRGLK 215
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SEQUENCE 26
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                           Lipoprotein.
SEQUENCE 4
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Q7YQQ0
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                                                                                                                                                                                                                                                                               [1] — SEQUENCE FROM N.A. MESUBORG SEQUENCE FROM N.A. MEDLINE-22761261; PubMed=12878460; Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.; Anrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.; A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003). EMBL; AF548420; AAP97376.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-22761261261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548424; AAP97380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zalophus californianus (California sealion).
Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pinnipedia, Otariidae, Zalophus.
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Pred. No. 14;
1; Mismatches 1; Indels
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80.0%; Pred. No. 14;
tive 1; Mismatches 1; Indels
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SEQUENCE 316 AA; 34540 MW; C04896B0E17562AE CRC64;
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SEQUENCE 318 AA; 34888 MW; C04E7ECBA8E64C96 CRC64;
                                                                                                                                01-0cT-2003 (TrEMBLrel. 25, Created)
01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 AA.
                                                                                                                                                                           Apolipoprotein B 100 (Fragment).
Name-apoB-100,
Nandinia binotata (African palm civet).
                                                                                                        PRT;
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162 SSLTRKRGLK 171
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160 SSLTRKRGLK 169
1 TDLTRKRGLK 10
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Matches 8; Conser
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Matches 8; Conserv
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                                                                                                                                                                                                                                                      Nandinia.
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Q7YQN9
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1 TDLTRKRGLK 10

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162 SSLTRKRGLK 171
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Search completed: January 13, 2005, 01:51:03 Job time : 79.0328 secs

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January 13, 2005, 01:14:40; Search time 69.4918 Seconds (without alignments) 46.460 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
                                                                                                                                                                                   US-09-823-418-15
44
1 TRLTRKGLK 9
                     Copyright
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB E
Maximum DB E
                                                                        OM protein
                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                              Run on:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:*geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* A_Geneseq_23Sep04:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aay30696 Apo-B100	Aay30694 Apo-B100			Abu02213 S. pneumo	Str	Aay55803 S. pneumo				Aaw57207 Apo B 100	Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b	-	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo
SUMMARIES	AAY30696	AAY30694	AAY30695	ADA47994	ABU02213	ADK46589	AAY55803	AAY30690	AAY30691	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400
DB	2	~	7	9	9	80	m	7	7	7	~	7	7	9	7	~	S	N	~	N	4	4	~	7	80
Length	6	0	σ	601	798	798	804	10	10	11	13	15	15	20	22	22	34	36	37	51	343	343	377	377	2463
% Query Match	100.0	93.2	86.4	77.3	77.3	77.3	77.3	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1
Score	44	41	38	34	34	34	34	33.5	33.5	33.5				33.5	33.5	٠	33.5	m	•	•	33.5	٠	33.5	٠	33.5
Result No.		7	3	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which amoulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apollo. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo assay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can

Aay31237 Human Apo Aaw41262 Apolipopr Aaw48685 Amino aci Aau98981 Human apo Add48677 Human Pro Aao1583 Human apo Abr40253 Human ali Abu79140 Apolipopr Adf43408 Apolipopr Adf43408 Human apo Adh18871 Human apo	Human Human Noval Apo-Bl Apo-Bl Lister Kiboso Riboso
AAY31237 AAW41262 AAW96826 AAU98981 AAD46677 AAO15893 ABC40253 ABC40253 ABC4040879140 ADF43408	AD033445 AD033447 AAU33184 AAX30700 AAX30698 AB49220 ADC89104 ADC89104
000000000000000000000000000000000000000	0884000777
66 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4563 4563 4563 4563 111 1147 1150 1151
76.11 76.11 776.11 776.11	76.1 76.1 75.0 75.0 75.0 75.0
	200000000000000000000000000000000000000
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 W W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                    Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                  Apo-8100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                   Claim 17; Page 57; 70pp; English.
                Ā
               AAY30696 standard; peptide; 9
                                                                                                                                                                                          98US-0077618P.
                                                                                                                                                                           99WO-US004805.
                                                                                                                                                                                                                              Boren JOS;
                                                 (first entry)
                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                              WPI; 1999-551509/46.
                                                                                                                                                                                                                           Innerarity TL,
                                                                                                             Synthetic.
Homo sapiens.
                                                                                                                                        W09946598-A1
                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                          10-MAR-1998;
                                                 17-NOV-1999
                                                                                                                                                         16-SEP-1999.
                                 AAY30696;
RESULT 1
         AAY30696
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Gaps

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Score 41; DB 2; Length 9; Pred. No. 1.7e+06; 1; Mismatches 0; Indels

93.2%; 88.98;

Query Match Best Local Similarity Sequence 9 AA;

8; Conservative

Matches

1 TRLTRKGLK 9

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TRLTRRGLK

AAY30695 standard; peptide; 9 AA.

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AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoBl00. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transpance on invivo model system for the etudy of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the conmation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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0
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                               ;
0
                                                                                                                                                                        Length 9;
                                                                                                                                                                                                           Indels
                                                                                                                                                                    100.0%; Score 44; DB 2; L
100.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        AAY30694 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                               1 TRLTRKGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-551509/46.
                                                                                                                                                                                                                                            TRLTRKGLK
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innerarity TL,
                                                                                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                              AAY30694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                      Query Match
                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                         RESULT 2
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compared to a 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which farupt LDL-PG binding with proteoglycan (PG). The method can be used for identifying compounds which farupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and manmals which carpounds which modulate atherosclerosis, and in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in a therosclerostic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the contact of a datherosclerostic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosts in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                        Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                            Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US004805.
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-551509/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999;
                                                                                                                                                                                                                                     17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                          AAY30695;
RESULT 3
AAY30695
LD AAY3
AAY30695
AAY3
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Gaps

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86.4%; Score 38; DB 2; Length 9; 77.8%; Pred. No. 1.7e+06; Live 2; Mismatches 0; Indels

1 TRLTRKGLK 9

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the experisitation (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the sequence of ABS5649. Also included are an antibody which binds one of the protein. treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 81-100 of a caquence contained within a Streptococcus nucleic acid sequence. The first primer is substantially complementary to the target sequence of the first primer is substantially complementary to the carget sequence contained within a Streptococcus nucleic acid sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes caid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus cand and antibiotics. The methods are useful for identifying media or ear infection. They are also useful in developing vectines, diagnostics and antibiotics. The methods are useful for identifying expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed sequence. Note: The sequence data for this patent did not form part of the printed protein and proteins or the present sequence is one of the 2469 proteins are defined by the identified coding regions from the genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.3%; Score 34; DB 6; Length 798; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3e+02;
0; Indels
                                                                           Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3582; 56pp; English.
                                                                                                                                                                                                                                                                                                                    Masignani V, Tettelin H, Fraser C;
                                                                                                                                                                                      27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                       27-MAR-2001; 2001GB-0007658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                      gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 RLTRKGL 162
                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-040579/03.
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                                                                                                             WO200277021-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ear infection.
                                                                                                                                                  03-OCT-2002
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ADK46589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substantially the same activity as the full-length polypeptide. The plypoptocitie of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a protein conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                            disease resistance; pathogen tolerance; plant pathogen; plant; rice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goff SA, Moughamer T;
icke D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%; Score 34; DB 6; Length 601; 87.5%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                       Rice protein conferring disease resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3, Cooper B, Goff SA Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 64; 299pp; English.
                                                                                                           ADA47994 standard; protein; 601 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU02213 standard; protein; 798 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2002; 2002WO-IB002453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2001; 2001US-0300112P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                    20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Briggs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glazebrook J, Brigge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRLTRSGL 270
|||||::|||
TRLTKRGLK 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 601 AA;
                                                                                                                                                                                                                                                                                                                                     WO2003000906-A2
                                                                                                                                                                                                                                                                                                Oryza sativa,
                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2003
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                                                                                                                                                  ADA47994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU02213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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ઠ 셤 us-09-823-418-15.rag

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This represents a S. pneumoniae priA polypeptide. The priA polypeptides and polynucleotides are useful for the treatment of microbial diseases (especially in the form of vaccines) and the methods are useful for identifying agonists and antagonists. The polypeptides are also useful for relating to diagnostic assays for detecting diseases associated with microbial infections (especially infections by Streptococcus pneumoniae) and conditions associated with such infections and assays for detecting priA expression or activity. The polypeptides are useful in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for screening of antibacterial drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                            New isolated priA polypeptides, useful for screening antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo-B100; proteoglycan receptor mutation; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.3%; Score 34; DB 3; Length 804 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                         St John A;
                                                                                                                                      Shilling L, Warren RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30690 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                         Claim 1; Page 4-5; 68pp; English
                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
                                                  99WO-US008771.
                                                                               98US-00067091.
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                                                                                                                                                                 WPI; 2000-062670/05.
N-PSDB; AAZ39569, AAZ39572.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 RLTRKGL 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 804 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLTRKGL
                                                  22-APR-1999;
                                                                                                                                       Mcdevitt D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1999
                                                                               27-APR-1998,
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                     02-DEC-1999
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                                                                                                                                                                                                                             compounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was sequence uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       priA polypeptide, microbial disease, vaccine, microbial infection, Streptococcus pneumoniae, antibacterial.
                                                                                                                                                                                                                                                                                                                                                          Houseweart CE;
                                                                                                                 Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                       Streptococcus pneumoniae protein, Seq ID No 3104
                                                                                                                                                                                                                                                                                                                                                         Opperman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 3104; 301pp; English
                                                                                                                                                                                                                                                                                                                                                       Bush D, Zeng Q,
ADK46589 standard; protein; 798 AA
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                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                               97US-0051553P.
98US-0085131P.
98US-00107433.

    S. pneumoniae priA polypeptide.

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                                                                                                                                               Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                02-JUL-1997;
                                                          20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening
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Matches
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                                                                                                AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which acceptor mutations. They were created to identify compounds which acceptor modulate atheroselerosels. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comports see detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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Pred. No. 3.8;
0; Mismatches 0; Indels
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                                                    Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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atherosclerosis,
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to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a therosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the compact of a particular food or drug composition tends to stimulate or inhibit the compact of the properties of the polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 3.8;
0; Mismatches 0; Indels
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Query Match
Best Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
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Length 13;

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This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids as . Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as . Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit amgiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits activation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
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                                                        Score 33.5; DE
Pred. No. 5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                AAW41261 standard, peptide, 15 AA.
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                                                        76.1%;
90.0%;
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                                                                                  Local Similarity
       Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                 AAW41261;
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                           Matches
                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                            8
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRGLK (2), or thair dimentially accorded to the competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                        ï
that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                     Score 33.5; DB 2; Length 11; Pred. No. 4.2; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW57207 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owens MD, Baillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                76.1%;
90.0%;
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                                                                                                                                                                                                                                                      9; Conservative
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                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                    TRLTRK-GLK
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                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                    Sequence 11 AA;
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Key Modified-Bite

Synthetic.

03-AUG-1998

AAW57207

RESULT 11 AAW57207

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Query Match

88888888

Best Loc Matches

WO9813385-A2

02-APR-1998

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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumaticid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                    Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.5; DB Pred. No. 7.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maynard HD;
                                                           Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2001; 2001US-0306726P.
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90.0%;
   (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TRLTRKRGLK 16
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(UYZU-) UNIV ZURICH.
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      10-MAY-2003
                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hubbell JA,
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      NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                            ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
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Pred. No. 5.8;
0; Mismatches
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                                                                                                                                                                                                            AAW96892 standard; peptide; 15 AA
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90.0%;
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                                        TRLTRKRGLK 10
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TRLTRK-GLK
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es 9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Best Loc Matches

RESULT 14 ABJ37575

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25-SEP-1997; 02-APR-1998.

97WO-GB002610. 96GB-00020153. 27-SEP-1996;

(UYST) UNIV STRATHCLYDE.

Baillie G; Halbert GW, Owens MD,

WPI; 1998-230637/20.

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Claim 13; Fig 7; 73pp; English.

The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 7 of identity with sequences: KABTKKNKHRH (1) or TTRLTRKRGIK (2), or their clienty with sequences: KABTKKNKHRH (1) or TTRLTRKRGIK (2), or their custul as: (1) drug-targeting vectors for delivering anticancer drugs to useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives coruring, receptor-competent LDL particles are considered apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor

Sequence 22 AA;

Gaps 1; Query Match 76.1%; Score 33.5; DB 2; Length 22; Best Local Similarity 90.0%; Pred. No. 8.7; Matches 9; Conservative 0; Mismatches 0; Indels

1 TRLTRK-GLK 9

7 TRLTRKRGLK 16

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SEQUENCE FROM N.A.
MEDLINE=98418625; PubMed=9747853;
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 SEQUENCE
                                                                                                                                                                                                                                                                                                        Q7WSQ9
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Q7WSQ9
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064892
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Q6fkt8 arabidopsis
Q6z55 oryza sativ
Bad10124 oryza sativ
Q8tjf9 methanosarc
Q8dmr6 streptococc
Q97pa5 streptococc
Q796a5 oryza sativ
Q8ru68 oryza sativ
Q7yqr5 aotus vocif
Q28473 macaca fasc
Q13788 homo sapien
P04114 homo sapien
Q7z600 homo sapien
Q7z600 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7wsq9 arthrobacte
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Q17274 brugia paha
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Aas95192 desulfovi
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Aat04728 listeria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               January 13, 2005, 01:15:45; search time 70.2295 Seconds (without alignments) 73.735 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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Q8dbu7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8y5x4
          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            1825181 segs, 575374646 residues
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Q9XBVS
Q92E67
AAS95192
SYS_PYRAE
Q9FKTB
Q6FKTB
Q65C5
Q625C5
Q8TJF9
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RS13 WUCBA
NDK ARCFU
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Listing first 45 summaries
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Q71<u>Y</u>86
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APB HUMAN
                                                                     - protein search, using sw model
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Q6BJK6
                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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seq length: 200000000
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                                                                                                                                                                                     1 TRLTRKGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                         UniProt_02:*
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Match Length
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                           Copyright
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Maximum DB :
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               091533 vibrio chol
094kz5 vibrio chol
087w29 pseudomonas
08pnk9 xanthomonas
939636 bacillus su
07p213 fusobacteri
06pej fusobacteri
06pej mus musculu
Aah57340 mus muscu
                                                                                                                                                                                                  Q80ys3 mus musculu
Q9qz09 mus musculu
Q9ums5 homo sapien
methanopyru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein (Pragment).
Ananas comosus (Pineapple).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
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 Q8tv10
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=43665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43696 MW; BB11CBADA85DF241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 19;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                       423 AA
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                                                                                                                                                                                                                                                                                              ALIGNMENTS
                 Q9L<u>5</u>33
Q9KKZ5
Q87WZ9
Q8PNK9
ROCC_BACSU
                                                                                                                                                                                                  Q80YS3
PHT1_MOUSE
PHT1_HUMAN
 NDK METKA
                                                                                                                          QBREI1
Q6PAP4
AAH57340
                                                                                                                                                                                   AAH60177
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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77.8%;
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064892;
01-AUG-1998 (TEMBLrel. 07,
01-AUG-1998 (TEMBLrel. 07,
01-OCT-2003 (TEMBLrel. 25,
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Best Local Similarity 77.8
Fr. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
 207 TRLTKOGLK 215
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Pred. No. 58;

77.8%;

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Best Local Similarity 77.8
Matches 7; Conservative
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Rellanz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Schlou-Mayer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA1599|IPF11452 Candida albicans IPF11452 of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Thomson K.G., Thomas J.E., Dietzgen R.G.; "Retrotransposon-like sequences integrated into the genome of
                                                                                                                                                                                                                                                                    GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0016740; F:Lransferase activity; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               871 AA; 100048 MW; EDFFD016E08952FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, CR382139; CAG90062.1; -.
SEQUENCE 453 AA; 50757 MW; DD4AF51CF5D956F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein, RNA-directed DNA polymerase, Transferase.
NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 36; DB 77.8%; Pred. No. 72; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                         le, Ananas comosus.";
ol. Biol. 38:461-465(1998).
12432; CAA73042.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00665; rve; 1.
Pfam; PF00078; RVT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 TRLTHKGVK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              871
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GENOLEVURES;
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Обвлк6;
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Matches
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Length 453;

DB 2;

79.5%; Score 35;

Query Match

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SEQUENCE FROW N.A.

SEQUENCE 1242'S DSM 30191;

Namination of the property of the prope
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  Indele
  1;
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                                                                                                                                                                                                               138 AA
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     Name=rbfA; OrderedLocusNames=CV1463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00003; -; 1.
InterPro; TPR0000238; Rib_bind_factA.
Pfam; PF02033; RBFA; 1.
ProDom; PD007327; Rib_bind_factA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseriaceae, Chromobacterium
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                                                                                                                                                                                                                                                                                                                                                                          Chromobacterium violaceum.
                                                                                                                                                                                                          STANDARD;
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368 SRLTRKGTK 376
                                         1 TRLTRKGLK 9
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SYS PYRAE
Q8ZTP4;
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AAS95192;
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                                                                                                                                                                                                                                                    Gaps
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Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales,
Desulfovibrionaceae, Desulfovibrio.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=mc2 155;
Bardou F., Martinez R., Puech V., Bleiber G., Prod'hom G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 77.3%; Score 34; DB 2; Length 172; Local Similarity 100.0%; Pred. No. 33; es 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         77.3%; Score 34; DB 1; Length 138; 100.0%; Pred. No. 26; ive 0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Amino acid ABC transporter, periplasmic-binding protein.
OrderedLocusNames=DVU0712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR155062; AAD12390.1; -.
Hypothetical protein
SEQUENCE 172 AA, 18622 MW; C4DFA92D0182E682 CRC64;
TIGRFAMS; TIGRO0082; rbfA; 1.
PROSITE; PS01319; RBFA; 1.
Complete proteome; rRNA processing.
SEQUENCE 138 AA; 15387 MW; E84750D86390272C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                             7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
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LTRKGLK 31
                                                                                                                                                                                                             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                3 LTRKGLK 9
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SEQUENCE FROM N.A.
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PubMed=15077118;

PubMed=15077118;

PubMed=15077118;

PubMed=15077118;

PubMed=15077118;

Rolonay J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,

Rolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,

Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,

Relson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,

Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;

The genome sequence of the anaerobic, sulfate-reducing bacterium

Desulfovibrio vulgaris Hildenborough.";
                                                                                                                                                                                                                                  Gaps
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10-OCT-2003 (Rel. 42, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
Name=serS; OrderedLocusNames=PAE3158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
8303).
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                                                                                                                                                                                2; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                  Indels
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11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Amino acid ABC transporter, periplasmic-binding protein.
                                                                                                      Complete proteome.
SEQUENCE 376 AA; 40203 MW; 14F0AFE97CC2B79B CRC64;
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Archaea, Crenarchaeota, Thermoprotei, Thermoproteales,
Thermoproteaceae, Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 AA
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                                                                                                                                                                             77.3%; Score 34; DB 87.5%; Pred. No. 80;
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InterPro; IPR001828; ANF_receptor.
InterPro; IPR000709; Leu_IIe_Val_bind.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00337; LEUILEVALBP.
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Biotechnol. 22:554-559(2004).
EMBL; AE017311; AAS95192.1; -.
TIGR; DVU0712; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2004 (TrEMBLrel. 27, 27-APR-2004 (TrEMBLrel. 27, 11-MAY-2004 (TrEMBLrel. 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.50,
Best and 7; Conservative
                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 130 RLTEKGLK 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=13773;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         120 rkirksci 127
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                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRKGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                1 TRLTRKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=B1142B04.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1142B04.27
                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- CATALYTIC ACTIVITY: ATP + L-Berine + tRNA(Ser) = AMP + diphosphate
+ L-seryl-tRNA(Ser).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned P1 and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Hypothetical protein
                                                                                                              -1- SUBCELLÚLAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
85-JUL-2004 (TrEMBLrel. 27, Last annotation update)
81milarity to cytochrome oxidase assembly factor (Hypothetical protein At5956090/MDA7 15)
Name-At5956090/MDA7 15, Synonyms-At5956090;
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 11, Erassicates; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2] SEQUENCE FROM N.A. Sekurai T., Akiyama K., Ishida J., Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98344145; PubMed-9679202;
Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                       Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0981; TRNASYNTHSER.
TIGRPAMS; TIGRO0414; serS; 1.
PROSTIE; PS50862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 AA; 52030 MW; 985B4C826E75D505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.3%; Score 34; DB 1; 75.0%; Pred. No. 98; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 AA.
                                                                                                                                                                                                                                                                                              HAMAP, WE 00176; -: 1
InterPro; IPR002314; TRNA-synt 2b.
InterPro; IPR002314; TRNA-synt 6er.
InterPro; IPR010978; TRNA-bindIng_arm.
InterPro; IPR006195; TRNA_1gase_II.
Pfam; PF03403; Seryl tRNA_1, 1.
Pfam; PF03803; TRNA_5bin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                     EMBL; AE009914; AAL64715.1; -. HSSP; P34945; 1SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches
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SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Onodera C.S., Quach H.L., Tang C., Tortumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative cytochrome c oxidase subunit 15(COX15) homolog isoform
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BAD10124;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
Putative cytochrome c oxidase subunit 15(COX15) homolog isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 482;
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87.5%; Pred. No. 1.18+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theologis A.; Series A.; Series A.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AB011476; BAB029291.1; Series AR117496; BAC42159.1; Series AR117496; BAC42159.1; Series AR117496; BAC42059.1; Series AR117496; BAC6029.1; Series AR117496; Series AR117496; Series Seri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Mataumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR005148; BAD10124-1; -.
InterPro; IPR003780; COX15, CtaA.
Pfam; PF02628; COX15, CtaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l protein.
457 Aa; 50127 MW; 6E7AODE6457E2DIE CRC64;
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Matches

RESULT 12

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Q8TJF9

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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:Hydrolase activity; IEA.
GO; GO:0003776; F:nucleic acid binding; IEA.
GO; GO:0015668; F:type III sitte-specific deoxyribonuclease ac. . .; IEA.
GO; GO:0009307; P:DNA restriction; IEA.
                                                                                                                                                                                                                                                       MEDLINE=21429245; PubMed=11544234; Hoskins J. Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
Tettelin H., Nelson R.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S.N., Heidelberg J.F., DeBoy K.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glass J.I.;
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                        Primosomal replication factor Y. Name-Entral, OrderedLocusNames-Epr1581, Streptococcus pneumoniae (Etrain ATCC BAA-255 / R6). Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te proteome; Helicase; Hydrolase.
90036 MW; DD0C4EEA5B269962 CRC64;
                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 2; Le
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          798 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008525; AAL00384.1; -.
PIR; C98069; C98069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO01410; DEAD.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01659; Pelicase_C.
InterPro; IPRO06935; Resili.
Pfam; PPO0271; Helicase_C; 1.
Pfam; PRO4851; Resili.; 1.
SMART; SMO490; HELICG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.3%; Scu-
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMB; TIGR00595; priA; 1.
ATP-binding; Complete proteome SEQUENCE 798 AA; 90036 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=SP1736;
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Best Local Similarity
7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 RLTRKGL 162
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                                                                                                                                                                                                  NCBI_TaxID=171101;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glass J.I
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=2219 (1972.23902;

K. MEDLINE=21929760; PubMed=11932.238; DOI=10.1101/gr.223902;

RA Galagan J.E., Nusbaum C., ROY A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A linton L., McKewan P., McKernan K., Talamas D.Y., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

Ra mphysiological diversity ",

Genome Res. 12:532-542(2002).

REMED, ABOILO94; AMMO7171; -.
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Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzae, Oryza, Oryza sativa.
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0
                                                                                                                                                 STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.3%; Score 34; DB 2; Length 493; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Length 482;
                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                        clone:B1142B04.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005148; BAD10124.1; -.
SEQUENCE 482 AA; 51446 MW; DC46727EC38CEAD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 AA; 56892 MW; 0170B5011675FD0C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                     Score 34; DB 2; I
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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(TrEMBLrel. 21, Last seq
(TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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TIGRFAMS; TIGR01630; psiM2_ORF9; 1.
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                                                                                                                                                                                                                                                                                                                       77.3%;
87.5%;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
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                                                                                                                           SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=39947;
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01-MAR-2003
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RESULT 13

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Length 798;

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Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angluoli S.V., Dickinson T., Hickey E.K., Holt I.E., Loftrus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Wing R.A., Yu Y., Yang T.J., Nah G., Soderlund C., Chen M., Kim H.-R., Rambo T., Saski C., Henry D., Oates R., Simmons J.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative 22 kDa kafirin cluster; Ty3-Gypsy type.
ORFNames=OSJNAb0075K12.33;
ORFNames=OSJNAb0075K12.33;
Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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EMBL; AC12148; AAM48279.1; -.
R EMBL; AC12148; AAM48279.1; -.
R InterPro; IPR001967; Pept_Aspartic.
R InterPro; IPR001969; Pept_Aspartic.
R InterPro; IPR001569; Retrocrans_gag.
R InterPro; IPR001584; Rve.
R InterPro; IPR00167; RVTse.
R InterPro; IPR001879; Znf_CCHC.
R InterPro; IPR001879; Znf_CCHC.
R Ffam; PF03732; Retrocrans_gag; 1.
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                                                                                                                                                                                                                                                                        Preumointage: ;

BMBL; AE007466; AAK75812.1; -.

R PIR; C95202; C95202.

R TIGR; SPT306; --

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016787; F:ATP-dependent helicase activity; IEA.

R GO; GO:0016787; F:ATP-dependent helicase activity; IEA.

R GO; GO:0003676; F:ATP-dependent helicase activity; IEA.

R GO; GO:0003676; F:ATP-dependent helicase activity; IEA.

R InterPro; IPR001410; DEAD.

R InterPro; IPR00150; Helicase_C.

R InterPro; IPR00150; Helicase_C.

R Pfam; PF00271; Helicase_C.

R SWART; SW00487; DEXDC; I.

R SWART; SW00490; HELICC; I.

R TIGREAMS;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.3%; Score 34; DB 2; Length 798; 100.0%; Pred. No. 1.9e+02; rative 0; Mismatches 0; Indels
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Matches 7; Conservative
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| 156 RLTRKGL 162
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SEQUENCE FROM N.A.
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1 TRLTRKERGLK 11
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1980s:*
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geneseqp2001s:*
geneseqp2001s:* A_Geneseq_23Sep04:* geneseqp2003bs:* geneseqp2004s:* .. 2 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	•	Aay30698 Apo-B100	Aay30700 Apo-B100				Aay30682 Apo-B100	Apo	Aaw57207 Apo B 100	Aaw41261 Apolipopr		Heba	80	ш	Aae14541 Human apo	Nucle	Aaw64587 Human apo	Aaw96845 Nucleic a		Abg52504 Human liv	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo	Human	Apolir	Aaw96826 Amino aci
SUMMARIES		AAY30698	AAY30700	AAY30697	AAY30699	AAY30690	AAY30682	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826
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% Query Match		100.0	94.4	85.2	81.5	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3	71.3				71.3	71.3	71.3	71.3	71.3
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Aau98981 Human apo Add48677 Human Pro Aao15893 Human apo Abr40253 Human ali		Human Human Novel Human	Ade45898 Human car Abg14088 Novel hum Abg06061 Novel hum Abb93444 Herbicida	Abp52170 Mouse pot Add37509 Mouse pho Adi27988 Murine pr Aay30683 Apo-B100
AAU98981 ADD48677 AAO15893 ABR40253	ABU79140 ADF43408 ADH18871 ADH18870	ADO33445 ADO33447 AAU33184 AAU21930	ADE45898 ABG14088 ABG06061 ABB93444	ABP52170 ADD37509 ADI27988 AAY30683
2729	9 7 8 8	8 8 4 4	C 4 4 D	2845
4560 4561 4563 4563	4563 4563 4563 4563	4563 4563 4590 97	97 270 1023 488	1095 1095 1095 10
71.3 71.3 71.3	71.3 71.3 71.3 71.3	71.3 71.3 71.3	70.4 70.4 70.4 68.5	66.7 66.7 66.7 65.7
38.38 38.53 38.53	38 38 38 38 38 38	38.5 38.5 38.5	9 9 9 P	36 36 35.5
222 284 298	33 33 33 33	3 3 5 7 5 7 5 6 7 5	38 38 44 10 10	4 4 4 4 2 2 4 5 2 6 4 5

ALIGNMENTS

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. AAY30698 standard; peptide; 11 AA. 98US-0077618P. 99WO-US004805. Innerarity TL, Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999. AAY30698; RESULT 1 **AA**Y30698

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Sequence 11 AA;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosele-rosals. The peptides are derived from amino acids 3358 to 3367 of apoblo0. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                         100.0%; Score 54; DB 2; Length 11; 100.0%; Pred. No. 0.0044; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                           Local Similarity 100.
nes 11; Conservative
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                                                                                                                                                                                                                                                                                         TRLTRKERGLK 11
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                                                                                                                                       Sequence 11 AA;
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Matches
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroscalerosis. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying also be used to identify compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the compounds the severity of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                      Gaps
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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     Length 11;
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   Score 51; DB 2;
Pred. No. 0.016;
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Pred. No. 0.13;
2; Mismatches
                                        1; Mismatches
                                                                                                                                                                                                AAY30697 standard; peptide; 11 AA.
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   94.4%;
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81.8%;
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Best Local Similarity 81.8%,
Best Local Similarity 81.8%,
                                                                                                                                                                                                                                                                    (first entry)
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Query Match
Best Local Similarity 90.9
Matches 10, Conservative
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                                                                         1 TRLTRKERGLK 11
                                                                                             1 TRLTRKDRGLK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which andulate atherosaclerosis. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the comment in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                     Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                       Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                           (first entry)
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Matches 10; Conservative
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TRLTRKE-GLK 10
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                               AAY30690;
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                     Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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Pred. No. 0.3;
1; Mismatches 1; Indels
                                                                                                                                          AAY30699 standard, peptide, 11 AA.
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81.8%;
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1 TRLTREKRGLK 11
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TRLTRDKRGLK
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
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16-SEP-1999.

AAY30699;

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Gaps

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Apo-B100 derived peptide showing a proteoglycan receptor mutation.

AAY30690 standard; peptide; 10 AA.

RESULT 5 AAY30690

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Matches

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97WO-GB002610.

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle of an apo B protein receptor and at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) and-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                              Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 52; 73pp; English.
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Best Local Similarity 90.>
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                                                                                                                                                                                                                                                                                                                 WPI; 1998-230637/20.
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                                          02-APR-1998,
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Apo-B100; proteoglycan receptor mutation, atherosclerosis,
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRKERGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                              Homo sapiens,
                                                                                                                                                              WO9946598-A1
                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                         10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998
                                                                                                                                                                                                                 16-SEP-1999
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                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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Matches
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Gape

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71.3%; Score 38.5; DB 2; Length 11; 90.9%; Pred. No. 3.1; 0; Mismatches 0; Indels

/note= "attached to retinoic acid"

Location/Qualifiers

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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRGLK (2), or their can be can be cancer cells that express an apo B protein receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.5; DB 2; Length 13;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FREE HOSPITAL SCHOOL MED.
                                                   Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                         Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96GB-00009702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1998 (first entry)
                (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRKERGLK 11
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TRLTRK-RGLK 12
                                                 Owens MD,
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                                                                                  WPI; 1998-230637/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNLO ) ROYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-1996;
                                                Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9743311-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW41261;
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Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity -

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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100) Z1-KAQ-X1-KWKHRHS-X2-T-Z2 (I) X1 = S or (Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 cc a. Compositions containing the peptide are used for simulteneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated compositions contained to reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits (factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW96878-97 represent nuclear localisation signal sequence derived from
used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.3%; Score 38.5; DB 2; Length 15; 90.9%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.2;
0; Mismatches
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                                                     60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96892 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suevara JG, Hoogeveen RC, Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Fig 13D; 293pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US011927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRKERGLK 11
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TRLTRK-RGLK 10
                                                     Disclosure; Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9856938-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1999
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Best Local S
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Gaps ï

0; Indels

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Apo B 100 binding site peptide analogue peptide C.

(first entry)

03-AUG-1998

AAW57208;

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AAW57208 standard; peptide; 22

RESULT 12

AAW57208

|||||| TRLTRK-RGLK 16

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human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (VLDL), intermediate density lipoprotein (IDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and postitively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                        Score 38.5; DB 2; Length 15;
Pred. No. 4.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                  fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                        71.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                          1 TRLTRKERGLK 11
                                                                                                                                                                                                                                                                                                                                                          6 TRLTRK-RGLK 15
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(UYZU-) UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-300420/29.
                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2003
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                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ37575;
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Matches
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: RAEYKANKHRH (1) or TYRLTRKRGIK (2), or their CC dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives CC for cell culture media especially as growth supplements. Non-naturally cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding comparing to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                            'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                            "attached to cholesterol"
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                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00020153.
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                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRKERGLK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1997;
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Best Local Simil
Matches 10; (
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                                                                                                                                                                                             Synthetic.
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Gaps

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71.3%; Score 38.5; DB 6; Length 20; 90.9%; Pred. No. 5.5; 0; Indels ive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 10; Conserv

Sequence 20 AA;

(first entry)

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New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                          Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                   Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ARKT-) ARK THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2001; 2001WO-GB003212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                                  WO200206314-A2
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                            peptide p62.
                                           17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lipoprotein.
                                                                                                                                                                                                                                                                                                                             24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Narvanen O,
AAE14541;
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density libeprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipephilic substituent. Also described in the cinvention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their CC dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                    Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.3%; Score 38.5; DB 2; Length 22; 90.9%; Pred. No. 6.1; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                               AAW57209 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230637/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9813385-A2
                                                                                                                                                                     03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halbert GW,
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                          AAW57209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                      RESULT 13
                                                             AAW57209
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Yla-Herttuala S;

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ij
The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunosassy to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothalial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollypoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.3%; Score 38.5; DE 90.9%; Pred. No. 9.4; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW96876 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRKERGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRLTRK-RGLK
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW96876
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1;

Gaps ;

10; Conservative 1 TRLTRKERGLK 11

Local Similarity

Best Loc Matches

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16

AAE14541 standard; peptide; 34 AA.

RESULT 14

AAE14541

Homo sapiens. WO9856938-A1

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AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major aportotein component of very low density lipoproteins (VLDL), intermediate density lipoprotein (VLDL), intermediate density lipoprotein sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                  Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                              Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                         97US-00874807.
98US-00079030.
                                                                                                                        98WO-US011927.
                                                                                                                                                                                                                                                                                 WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36 AA;
                                                                                                                                                         13-JUN-1997;
                                                                                                                                                                             14-MAY-1998;
                                                                                                                      10-JUN-1998;
                                                                                     17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                    treatment.
```

1; Query Match 71.3%; Score 38.5; DB 2; Length 36; Best Local Similarity 90.9%; Pred. No. 9.9; Matches 10; Conservative 0; Mismatches 0; Indels ð

ı,

Gaps

|||||| |||| 11 TRLTRK-RGLK 20 1 TRLTRKERGLK 11 쉽 Search completed: January 13, 2005, 01:43:04 Job time : 86.1011 secs

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version 5.1.6
- 2005 Compugen Ltd.
 GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

Run on:

January 13, 2005, 01:30:05; Search time 15.8689 Seconds (without alignments) 66.696 Million cell updates/sec

US-09-823-418-17 54 1 TRLTRKERGLK 11 Title: Perfect score: Scoring table: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bimE protein - Eme		apolipoprotein B-1	glucosyltransferas	hypothetical prote		_		•		hypothetical prote	apolipoprotein B-1	apolipoprotein B -	arginine transport	hypothetical prote	gag polyprotein -	hypothetical prote					α	hypothetical prote	•н	ropy-2 protein [im	protein	4	_	_
SUMMARIES	ID	BWASBE	S32802	LPHUB	T49903	H84008	D98082	AI2112	C72305	A36950	S49963	AC1031	C60950	JH0102	B64188	A69843	A46312	T25791	T38787	G82319	NKVLHH	T13447	AF0547	T04197	AF2471	T46589	E60950	S47102	G75409	H72645
	<u> </u>							~																						
	Query Match Length	1 7	296	4563	488	248	250	264	405	100	346	807	269	779	221	250	608	191	246	284	305	332	541	605	643	710	275	100	132	150
di	Query Match	77.8	71.3	71.3	68.5	66.7	66.7	66.7	66.7	64.8	64.8	64.8	63.9	63.9	63.0	63.0	63.0	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	•	60.2	6	٥.	ė.
	Score	42	œ.	38.5	37	36	36	36	36	35	35	35	34.5	4.	34	34	34	33	33	33	33	33	33	33	33	33	32.5	32	32	32
	Result No.		7	e	4	ហ	9	7	80	Q,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

hypothetical prote	response requiator	hypothetical prote	hypothetical prote	heterodisulfide re	hypothetical prote	hypothetical prote	hypothetical prote	nucleocapsid prote	cytosolic axial fi	hypothetical prote	glutamate-cysteine	glutamate-cysteine	hypothetical prote	competence protein	translation elonga	
G84502	A75287	F95218	AB1827	AF2223	T48758	S40752	E83723	JQ2191	D70410	T00484	JH0611	A35015	T29177	A12053	805988	CHICLESCO
7	7	N	~	7	~	7	~	~	~	7	7	7	~	~	8	
202	220	250	366	301	345	398	429	441	458	627	637	637	771	798	844	
59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
RESULT 1

BWASBE

DAMASBE

DAMS BE

C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

R; Engle, D. B.; Osmani, S.A.; Osmani, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R.

A; Title: A negative regulator of mitosis in Aspergillus is a putative membrane-spanning A; Molecule type: mRNA

A; Reference number: A37879

A; Molecule type: mRNA

A; Residues: 1-2073 < ENG>
A; Molecule type: mRNA

A; Residues: 1-2073 < ENG>
A; Note: in addition to three predicted transmembrane domains, there are several potent) assent kinase, and one sequence that resembles a nuclear localization signal

C; Comment: This protein is part of a regulatory pathway that includes the nimA protein c; This protein is part of a regulatory pathway that includes the nimA protein C; Genetics:

A; Genetics:

C; Genetics:

A; Genetics:

A; Genetics:

C; Genetics:

A; Genetics:

C; Superfamily: bimE protein

C; Superfamily: bimE pro
```

ö DB 1; Length 2073; 0; Indels Score 42; DB 1 Pred. No. 14; 2; Mismatches 77.8%; Query Match
Best Local Similarity 80.0
Matches 8; Conservative

ö

Gaps

|||||::||| 832 TRLTRRKRGL 841 1 TRLTRKERGL 10 ò g

RESULT 2 S32802

apolipoprotein B - crab-eating macaque (fragment)
Cispecies: Macaca fascicularis (crab-eating macaque)
Cispecies: Macaca fascicularis (crab-eating macaque)
Cispecies: Macaca fascicularis (crab-eating macaque)
Cispacies: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
Ciscossion: 832802
M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melch, Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional 1 A;Reference number: 832802; MUID:92075708; PMID:1742325
A;Accession: 832802
A;Accession: 832802
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-596 cPAP>
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g93001
C;Superfamily: apolipoprotein B

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A;Residues: 485-617, A', 619-1044 cLA2>
A;Cross-references: GB:M12480; NID:g178791; PIDN:AAA51751.1; PID:g178792
A;Cross-references: GB:M12480; NID:g178791; PIDN:AAA51751.1; PID:g178792
R;Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; K
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A;Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipop
A;Reference number: A94088; MUID:86149325; PMID:3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Accession: A25774
A.Molecule type: mRNA
NIS TO STORES
A.GENERAL TO STORES
A.GENERAL TO STORES
A.MOLECULE TO STORES
A.MOLECULE TYPE TO STORES
A.MOLECULE TYPE TO STORES
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A, Residues: 'N', 3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 3:
A, Residues: 'N', 3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 3:
A, Cross-references: GB:M12413; NID:G178735; PIDN:AAA11742.1; PID:G178736
R; Chen, S. H.; Habib, G:, Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Ca. Science 238, 363-366, 1987
A; Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific is A; Reference number: A40133; MUID:88018019; PMID:3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Accession: A40133

A/Molecule type: protein

A/Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-5:

36;1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-

A/Note: these fragments were derived from apo48

R/Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 2165-2179 <CH1>
A;Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A;Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:M12681; NID:g178797; PIDN:AAA51753.1; PID:g178798 R; Deeb, S. S.; Mctulsky, A.G.; Albers, J.J.
R; Deeb, S. S.; Mctulsky, A.G.; Albers, J.J.
R; Deeb, S. S.; Mctulsky, A.G.; Albers, J.J.
A; Title: A partial cDNA clone for human apoliprocein B.
A; Reference number: A25774; MUID:85270450; PMID:3860836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-291 <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A25774
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A; Residues: 1-617, A', 619-1929, F', 1931-3318, D', 3320-3426, T', 3428-3431, 'Q', 3433-3731,'
A; Cross-references: UNIPROT: P04114; UNIPROT: P78482; UNIPROT: P78479; UNIPROT: Q9UMNO; UNIE
R; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A; Reference number: A91058; MUID: 87161758; PMID: 3030729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA 519-703,'P',705-792,'R',794-1270,'S',1272-1866,'G',1868-2036,'N',2 4188-4220,'M',4122-4563 a.LAW> 4189-4220,'M',4222-4563 a.LAW> 4189-4220,'M',4222-4563 a.LAW> 4189-4220,'M',4222-4563 a.LAW> 4189-4220,'M',4222-4563 a.LAW> 4189.4220,'M',4222-4563 a.LAW> 4189.4220,'M',4222-4563 a.LAW> 4189.4220,'M',522-4563 a.LAW> 4180-4220,'M',5210,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-418,'M',700-41
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A, Residues: 1-11.15-239,/S',2541-3823,'R',3825-4563 <CLA>
A, Residues: 1-11.15-239, Gound
A, Note: 1109-Asp was also Gound
B, Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McCa
R, Knott, T.G.; Wallis, S.C.; Powell, E.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McCa
N, Moleic Acids Res. 14, 7501-7503, 1986
A, Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A, Reference number: A93639; MUID:87016385; PMID:3763409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A27850; A25679; A22567; A25266; A24520; A24684; A23817; A25774; A26
A52; IS1099; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scc
DNA 6, 363-372, 1987
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A; Residues: 1-272, N', 274-617, A', 619-1217, E', 1219-2091, V', 2093-2364, T', 2366-2679, 'Q'
A; Cross-references: GB:X04506; NID:g34330; PIDN:CAA28191.1; PID:g34331
R; Law, S.W.; Grant, S.M.; H; H; Houchi, K.; Hospettankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Titles: Human liver apolipoproceain B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
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A; Residues: 1-97, 17, 99-328, VV, 330-644, I', 646-918, P', 920-3318, D', 3320-3426, T', 3428-

B, 4132, G', 4134-4180, E', 4182-4563 (CHE)

A; Cross-references: GB: J02610; NID: g178803; PIDN: AAA35549.1; PID: g178804

A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides

B; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H

Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986

A; Title: Analysis of CDNA clones encoding the entire B-26 region of human apolipoprotein

A; Accession: A24320; MUID: 86287319; PMID: 3461454
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A; Residues: 1-97, 1', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138,' PTGRLENCFSNGLICYSLWLHSFQE
A; Cross-references: GB:M14081; NID:g1795; PIDN:AAAS1752.1; PID:g553189
R; Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A; Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                  1,
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein B-100 precursor - human
N/Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
                                                                                                                                  ;
            Length 596;
                                                                                                                            Indels
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            7
            BB
Score 38.5; DE
Pred. No. 21;
0; Mismatches
71.3%;
90.9%;
                                                                                                                      10; Conservative
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TRLTRK-RGLK 235
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                                                 Best Local Similarity
Matches 10; Conser
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Query Match
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Gaps

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glucosyltransferase-like protein - Arabidopsis thaliana
NiAlternate names: protein T24H18.60
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-dun-2000 #sequence_revision 02-dun-2000 #text_change 09-Jul-2004
C;Accession: T49903
R;Bevan, M; Robben, J; Grymonprez, B.; Volckaert, G.; Bancroft, I.; Mewes, H.W.; Rudd
Submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein BH2872 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H84008
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84008
A;Status: preliminary
A;Molecule type: DNA
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A,Cross-raferences: UNIPROT:09K8Y0; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06
A,Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T49903
A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-488 EBEV>
A;Cross-references: UNIPROT:Q9LXVO; EMBL:AL353013; GSPDB:GN00063; ATSP:T24H18.60
A;Experimental source: cultivar Columbia; BAC clone T24H18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 36; DB 2; Length 248; llarity 88.9%; Pred. No. 28; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 488;
                                     0; Indels
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          Pred. No. 1.3e+02;
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Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1
                                     0; Mismatches
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C;Superfamily: flavonol 03-glucosyltransferase
   90.98;
                                                                                                                                                 3385 TRLTRK-RGLK 3394
      Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                        1 TRLTRKERGLK
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nes 8; Conserv
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A; Residues: 2169-2179 <HOS>
A; Residues: 2169-2179 <HOS>
A; Residues: 2169-2179 <HOS>
A; Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250K apoB-48, CAA encoding 2180-GIn is substituted by the stop codon TAA, R; Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
A; Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human application and characterization of sulfhydryl and disulfide peptides of human application disulfide bonds
   124
                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
A, Residues: 3056-3159 <MEH>
A, Residues: 3056-3159 <MEH>
B, Crose references: GB:X03045, NID:g28783, PIDN:CAA26850.1; PID:g929609
R, HOSpattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A;Title: Identification of a novel in-frame translational stop codon in human intestine
A, Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
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                                                                                              A, Molecule type: mRNA
A;Residues: 2129-2179, 2181-2235 <HA2>
A;Cross-references: GB:M18471
A;Experimental source: intestine
A;Note: this mRNA from intestine includes a stop codon created by RNA editing in place of the mRNA from intestine includes a stop codon created by RNA editing in place of the mRNA from intestine includes a stop codon created by RNA editing in place of the mRNA from intestine includes a stop codon created by RNA editing in place of the mRNA schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, Shucleic Acids Res. 13, 6937-6953, 1985
A;Title: Human apolipoprotein B: identification of cDNA clones and characterization of rakeference number: A24269; MUID:86041888; PMID:3303660
A;Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism ; A;Reference number: A28002; MUID:88106542; PMID:3426612 A;Accession: A28002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.B.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A22006
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Gaps

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Gaps

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71.3%; Score 38.5; DB 1; Length 4563;

Query Match

us-09-823-418-17.rpr

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Gaps

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Length 405

DB 2;

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A;Molecule type: DNA
A;Residues: 1-346 <SKE>
A;Cross-references: UNIPROT:P40546; EMBL:Z46881; NID:G599967; PIDN:CAA86973.1; PID:G599
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-100 <MAE>
A;Cross-references: UNIPROT:Q07399; GB:D14439; NID:g393296; PIDN:BAA03323.1; PID:g21636
C;Superfamily: urease, gamma subunit; urease 11K chain homology
C;Keywords: hydrolase
F;1-100/Domain: urease 11K chain homology <U11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urease (EC 3.5.1.5) 11k chain - Bacillus sp. (strain TB-90)
NyAlternate names: ureA protein
C;Species: Bacillus sp.
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A36950
R;Maeda, M.; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
J;Bacteriol. 176, 432-442, 1994
A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90
A;Reference number: A36950; MuID:94117379; PMID:8288539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YIL019w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YI3299.12
C;Species: Saccharomyces cerevisiae
C;Dapeies: 28-May.1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: S49963
R;Skelton, J.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A;Reference number: 849951
A;Reference number: 849951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.8%; Score 35; DB 2;
100.0%; Pred. No. 19;
ive 0; Mismatches
                                                                                                                                                               Score 36; DB 2
Pred. No. 44;
2; Mismatches
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Pred. No. 59;
3; Mismatches
         A,Experimental source: strain MSB8
C,Generica:
A,Gene: TW104
C,Superfamily: hypothetical protein b1432
                                                                                                                                                               66.7%;
70.0%;
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60.0%;
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A,Cross-references: SGD:S0001281
A,Map position: 9L
                                                                                                                                   Query Match
Best Local Similarity 70.v.
7, Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                        227 RISRKORGSK 236
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298 KATKRERGLK 307
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AC1031
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A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Status: DNA
A,Residues: 1-264 «KUR»
A,Cross-references: UNPROT;Q8YU98; GB:BA000019; PIDN:BAB74155.1; PID:g17131548; GSPDB:G
A,Cross-references: strain PCC 7120
C,Genetics:
A,Gene: all2456
C,Superfamily: conserved hypothetical protein H10188
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A,Molecule type: DNA
A,Residues: 1-405 <ARN>
A,Cross-references: UNIPROT:Q9X0D4; GB:AE001764; GB:AE000512; NID:g4981561; PIDN:AAD3612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein all2456 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: Al2112
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Thermotoga maritima
C;Species: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72305
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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RiHoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; I. LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I. J. Sun, P.M.; Winhler, M.E.
J. P.; Sun, P.M.; Winhler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250 «KUR»
A;Residues: 1-250 «KUR»
A;Cross-references: UNIPROT:QBDNJ3; GB:AE007317; PIDN:AAL00489.1; PID:g15459361; GSPDB:
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A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72305
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C, Superfamily: inner membrane protein malk, ATP-binding cassette homology
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124 LTRRERGL 131
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A; Contents: annotation
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hypothetical protein STV4573 [imported] - Salmonella enterica subsp. enterica serovar Typi C,Species: Salmonella enterica subsp. enterica serovar Typii A,Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AC1031
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., Connercon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A,Reference number: AB0502; MUID:21534947; PMID:11677608
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Cispecies: Masocricetus auratus (golden hamster)
Cispecies: Masocricetus auratus (golden hamster)
Cispecies: Masocricetus auratus (golden hamster)
Cispecies: Scott, J.
3. Lipid Res. 31, 1109-1120, 1990
Airlile: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A,Reference number: A60950; MUID:90324804; PMID:2373961
A,Reference number: A60950
A,Residues: 1-269 cLAN>
A,Residues: 1-269 cLAN>
A,Residues: 1-269 cLAN>
A,Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C; Superfamily: apolipoprotein B
C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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submitted to GenBank, June 1990
A;Reference number: A38864
A;Accession: JH0102
A;Molecule type: DNA
A;References: UNIPROT:Q60536; GB:M35187
A;Note: this is a revision to the sequence from reference JH0101
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
A;Note: this is a revision to the sequence from reference JH0101
A;Note: this is a revision to the sequence from reference JH0101
A;Note: this is a revision to the sequence from reference JH0101
A;Note: this is a revision to the sequence from reference JH0101
A;Note: this is a revision to the sequence from reference JH0101
A;Reference number: JH0101; MUID:90236327; PMID:2332175
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-807 <PAR>
A; Cross-references: GB:AL513382; PIDN:CAD09348.1; PID:g16505348; GSPDB:GN00176
C; Genetics:
A; Genetics:
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr.1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
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Pred. No. 1.3e+02;
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81.8%; Pred. No. 59;
tive 1; Mismatches
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77.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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508 RLTRADRGL
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arginine transport system permease protein artQ - Haemophilus influenzae (strain Rd KW; C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: B-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C; Accession: B64188
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, GGozyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
A; Authors: Grahm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reterence number: A64000; MUID:95350630; PMID:7542000
A; Reterence number: A64000; MUID:95350630; PMID:7542020; NID:91574095; PIDN:AAC22829.1
C; Genetics:
A; Reterence arto
C; Genetics:
A; Description: probably required for transhocation of the substrate across the membrane C; Superfamily: histidine permease protein
C; Superfamily: histidine permease protein
C; Superfamily: histidine permease protein
F; 4-20/Domain: transmembrane #status predicted <TMI>F; 50-66/Domain: transmembrane #status predicted <TMI>F; 50-66/Domain: transmembrane #status predicted <TMI>F; 50-66/Domain: transmembrane #status predicted <TMI>F; 190-206/Domain: transmembrane #s
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C;Species: Bacillus subtilis
C;Accession: A69843
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
                                                                                                                                                                                                          cholesterol metabolism; chylomicron; glycoprotein
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Pred. No. 61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      63.9%; Score 34.5; DB 2; Length 781.8%; Pred. No. 1.5e+02; ive 1; Mismatches 0; Indels
A,Note: this sequence has been revised in reference A38864 (Genetics: A,Genetics: A,Genetics: C,Superfamily: apolipoprotein B C,Superfamily: apolipoprotein B C,Superfamily: apolipoprotein B C,Steywords: atherosedlerosis; calcium; cholesterol metaboli: F,435-445/Region: receptor binding F,646-656/Region: receptor binding
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70.0%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winger, A.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Authors: Yoshikawa, H.F.; Zumateain, E.; Yoshikawa, H.; Danchin, A.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69843
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-250 «KUN»
A;Residues: UNIPROT:031597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998.
C;Genetics:
A;Gene: YjbA
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63.0%; Score 34; DB 2; Length 250;
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Matches 7; Conservative 1; Mismatches 1; Indels
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Q82b17 streptomyce
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Compugen Ltd.
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                      GenCore version (c) 1993 - 2005
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Q6ZEZB
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Maximum Match 100%
Listing first 45 summaries
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Q7YQRS
Q28473
Q13788
APB_HUMAN
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Q7U8V5
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Q6HM04
Q73BX2
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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54
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Perfect score:
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Maximum DB
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32 35 64.8 210 2 QTRYL3 Q7ryl3 neurospora 33 35 64.8 259 2 Q88UG3 Q881g3 pseudomonas 34 35 64.8 281 2 Q72NN4 Q881g3 pseudomonas 35 64.8 281 2 QRF989 Q872NN4 Q881g3 pseudomonas 36 64.8 281 2 AA568890 Aa668890 leptospira 37 35 64.8 322 2 Q6CU76 G6CU76 G6CU76 Kluyveromyc 39 35 64.8 345 1 DDL WOLSU Q7ma71 wolinella s 40 35 64.8 346 1 DDL WOLSU G7ma71 wolinella s 41 35 64.8 346 2 AA556415 G6G55 saccharomyc 42 35 64.8 346 2 AA556415 G6G55 saccharomyc 44 35 64.8 438 2 Q99JK2 Q99JK2 Q99JK2 M9EU17 oryza sativ
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ALIGNMENTS

BIME EMENI ID BIME EMENI STANDARD; PRT; 2073 AA.	
01-MAR-1992 (Rel.	
(Rel	
Negative regulator of mitos	
OC BUIOTIALES; Trichocomaceae; Emericella. OX NCRI TaxID=162425:	
MEDLINE=90375468; PubMed=1697851;	
RA Engle D.B., Osmani S.A., Osmani A.H., Rosborough S., Xiang X., RA Morris N.R.:	
membrane-spanning protein.";	
н 	
CC -:- FUNCTIONS NEGACITY REQUISION OF MICOSIS IN E. MICOLIONS INSECUCIONS TO A PART OF A PART O	
mitosis. Mutations to this protein both cause cells	
mitosis and prevent	
-!- SIMILARITY: Contains 4 PC repeats.	
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InterPro; IPR002015; AF	
Pfam, PF01851; PC	
KW MICOBIB; Kepear; Transmembrane. FT DOMAIN 342 353 Nuclear localization gional (Dotential)	
TRANSMEM 1623 1643 Potential.	
TRANSMEM 1685 1703	
TRANSMEM 1746 1764 Potential.	
SQ SEQUENCE 2073 AA; 229178 MW; 05E4E81EADDF51E4 CRC64;	
77.8%; Score 42;	
Best Local Similarity 80.0%; Pred. No. 56; Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps (0;
OV 1 TRLIRKERGL 10	

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Q7YQR5 Q7YQR5;

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SECURNCE FROM N.A.
MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein B-
 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P04114; 000502; 013787; 01.703 pr.; 01.703 pr.; 01.804.1386 (Rel. 03, Created) 01.80V-1986 (Rel. 03, Last sequence update) 01.80V-1986 (Rel. 44, Last amortation update) Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein publication update]
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87191999; PubMed=2883086; MEDLINE=87191999; PubMed=2883086; Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.; Carlsson P. the human apolipoprotein B gene; complete structure of "Analysis of the human apolipoprotein B gene; complete structure of the B-74 region."; Gene 49:29-51(1986). BMEL; MISS-39-51(1986). BMEL; MISS-39-51(1986). Cextracellular; NAS. GO; GO:0005576; Cextracellular; NAS. GO; GO:0005869; F:lipid transporter activity; NAS. GO; GO:0006869; P:lipid transport; NAS.
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MEDLINE=88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
DNA 6:363-372(1987).
                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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   Indels
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Last annotation update)
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Pred. No. 4.8e+02;
0; Mismatches 0;
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 Mismatches
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Conservative
                                                                     TRLTRK-RGLK 235
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                   1 TRLTRKERGLK 11
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Name=APOB;
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10;
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Matches
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
An ew phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AF548396; AAP97352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Apolipoprotein B (Fragment)
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E., Marctti K.R., Melchior G.W.;
"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                414 414 414 414 4A; EEFA8492157E1BDE CRC64;
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66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
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Pred. No. 50;
0; Mismatches
                                                                   414 AA
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Pred. No. 74;
                                                                                                     Created)
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MEDLINE-92075708; PubMed=1742325;
                                                                                                                                                        Apolipoprotein B 100 (Fragment).
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90.9%;
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PIR; S32802; S32802.
                                                               PRELIMINARY;
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596
596 AA;
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Best Local Similarity
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"The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86041888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.;
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characterization of mRNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
MEDLINE=86093680; PubMed=3841204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schilling J.W., Yamanaka M.,
                                                                                                               SEQUENCE FROM N.A.
MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Law S.W., Brewer H.B. Jr.;
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derived amino acid sequence.";
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MEDIJINE-86287319; PubMed=3461454;
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Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O., Bjursell G.;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=87161788; PubMed=3030729;
Cladarae C., Hadzopoulou-Cladarae M., Nolte R.T., Atkinson D.,
Zannis V.I.;
             AND VARIANTS ILE-98 AND GLU-4181
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MEDLINE=85270450; PubMed=3860836;
Deeb S.S., Motulsky A.G., Albers J.J.;
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Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
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PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
                                                                                         Biol. Chem. 261:12918-12921(1986).
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MEDLINE-88018019; PubMed-3659919; Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H., Silberman S.R., Cai S.-J., Deelypere J.P., Rosseneu M., Gotto A.W. Jr., Li M.-H., Chan L.; Apolipoprotein B-48 is the product of a messenger RNA with an organspecific in-frame stop codon.";
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AND THR-4481.
MEDLINE-97044521; PubMed-8889592;
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WEDLINE=95190020; PubNed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.
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Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
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intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM-BINDING DATA.
MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B is a calcium binding protein.";
Biochem. Biophys. Res. Commun. 137:493-499(1986).
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Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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MEDLINE=91071750; PubMed=1979313;
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                                                                                                                                                                                           specific in-frame stop codon.";
Science 238:363-366(1987).
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Last sequence update) Last annotation update)

Created) PRT;

431 AA

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MEDLINE-22825697; PubMed=12917641; DOI=10.1038/nature01943; MEDLINE-22825697; PubMed=12917641; DOI=10.1038/nature01943; Patenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; "The genome of a motile marine Synechococcus."; "The genome of a motile marine Synechococcus."; Mature 424:1037-1042(2003).

EWBL; BX569690; CABO7101.1; "GO; GO:0005525; F:GTP binding; IEA.

ILGERPO; IRRO5525; Small GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                    431 AA; 47647 MW; 666ECD647A83217D CRC64;
                                                                                                                                                                  OrderedLocusNames=SYNW0504;
Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                           (TrEMBLrel. 25,
         3385 TRLTRK-RGLK 3394
                                                                                 PRELIMINARY;
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                                                                                                                                                                                                              NCBI_TaxID=84588;
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Q7U8V5;
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MEDLINE=97403938; PubMed=9259199;
Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krempf M., Giraudet P., Junien C., Boileau C.,
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detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
PCR-SSCP.",
Hum. Mutat. 8:282-285(1996).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
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InterPro; IPR001747; Lipid transprt_N. Pfam; PF06448; DUF1081, 1.
Pfam; PF01347; Vitellogenin_N; 1.
SMART; SM00638; LPD_N; 1.
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                                                                                                                                                                                         Hum. Mutat. 10:160-163(1997).
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Best Local Similarity 90.99
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SEQUENCE 4
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyte; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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68.5%; Score 37; DB 2; Length 431; 77.8%; Pred. No. 1e+02; ive 2; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glucosyltransferase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               488 AA
                                         Best Local Similarity 77.8
Matches 7; Conservative
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STRAIN=97-27;
Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AR017355; AAT63074.1;
Interpro; IPR010983; EF_Hand_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D., "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pxOl."; Nucleic Acids Res. 32:977-988 (2004).
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                                                                                                                            2; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
ORFNames=BT9727_1080,
Bacillus thuringiensis serovar konkukian str. 97-27.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus thuringiensis serovar konkukian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEOUENCE 248 AA; 30052 MW; 4C44DCDD6B421736 CRC64;
  Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005956; BAC51026.1; -.
CCMplete proteome.
SEQUENCE 94 AA; 10344 MW; 4925ED8E76A04BB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                               248 AA
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32;
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88.9%; Pred. No. 91;
iive 0; Mismatches
                                                                                                                                                                   1; Mismatches
                                                                                                                            Score 36;
Pred. No.
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                                                                                                                                            87.5%;
                                                                                                                          66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=BCE1296;
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Best Local Similarity 88.5
Secondary 88.5
                                                                                                                        Query Match 66.7
Best Local Similarity 87.5
Matches 7; Conservative
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86 RLTREERG 93
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05-JUL-2004
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Q6HM04
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Arabidopsis thalīana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
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  Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%; Score 37; DB 2; Length 488; 77.8%; Pred. No. 1.2e+02; ive 1; Mismatches 1; Indels
                                         1; Indels
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                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
Score 37; DB 2; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                           488 AA
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                                         1; Mismatches
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  68.5%;
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OrderedLocusNames=bs15761;
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                                         Conservative
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les 7, Conservative
                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                2 RLTRKERGL 10
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                  Local Similarity
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  Query Match
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Q89178
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                                                                    Nature 423:81-86(2003).
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SEQUENCE FROM N.A.
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Horikoshi K.;
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
"Genome sequence of Bacillus cereus and comparative analysis with
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STRAIN=Ames / isolate Porton;
MEDLINE=2260414; PubMed=12721629; DOI=10.1038/nature01586;
MEDLINE=2260414; PubMed=12721629; DOI=10.1038/nature01586;
Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonsy J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
DOBSOY R.T., Madpu R., Daugherty S.C., Durkin A.S., Haff D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
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                                         2; Length 248;
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                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=BC1176;
Bactllus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillus.
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NCBI_TaxID=1392;
Complete proteome; Hypothetical protein, SEQUENCE 248 AA; 30064 MW; 2EC2A2C58C7CA2EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 423:87-91(2003).
EMBL; AB017001; AAP08163.1; -.
InterPro; IPR010983; EF.Hand_like.
Hypothetical protein.
SEQUENCE 248 AA; 29788 MW; 79EBCC5746C2BDA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=BA1187, BAS1098; ORFNames=GBAA1187;
                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
                                    66.7%; Score 36; DB
88.9%; Pred. No. 91;
ive 0; Mismatches
                                                                                                                                                                           248 AA
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                       Ouery Match
Best Local Similarity 88. ی
و Conservative
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Q81GL8;
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Ames / isolate 0581;
STRAIN=Ames / isolate 0581;
STRAIN=Ames / isolate 0581;
STRAIN=Ames / isolate 05.4.; Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
"Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Stichardson P., Rubin E., Tice H.; Longmire J., Lucas S., Okinaka R., Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AR017027, ABPS150.1; -

EMBL, AR017225; AAT50275.1; -

EMBL, AR017225; AAT51421.1; -
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EMBL, AP001516; BAB06591.1; -.
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Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolstoe A.B., Fraser C.M.; "The genome sequence of Bacillus anthracis Ames and comparison closely related bacteria.";
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Pred. No. 91;
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Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; PRO10983; EF_Hand_like.
Hypothetical protein.
SEQUENCE 248 AA; 30052 MW; 4C44DCDD6B421736 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
BH2872 protein.
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88.9%; Pred. No. 91;
ive 0; Mismatches
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Search completed: January 13, 2005, 01:51:08 Job time : 88.8361 secs

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January 13, 2005, 01:14:40; Search time 84.9344 Seconds (without alignments) 46.460 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                 2002273 seqs, 358729299 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp1990s:*
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geneseqp2003as:*
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geneseqp2001s:*
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seq length: 200000000
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                  Copyright
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Perfect score:
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                                                                                                                                                                                                                                                                                 Searched:
                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description						-		-	Aaw57205 Apo B bin		Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b		Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abq52504 Human liv	Aar72704 Human apo		Adj57400 Human apo	Human
SUMMARIES	ID	AAY30700	AAY30698	AAY30697	AAY30699	AAY30683	AAY30691	ABU24550	ADN47108	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237
	DB	5	~	~	N	~	~	9	80	ď	~	~	~	9	N	7	2	~	N	~	4	4	N	~	∞	7
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,	* Query Match	100.0	92.7	80.0	76.4	71.8	71.8	70.9	70.9	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0		70.0	•	70.0
	Score	55	51	44	42	9.	39.5		39	38.5	8	38.5	38.5	38.5		38.5	•	В.		38.5	ω.	œ.			38.5	ω.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate acherosclerosis. The peptides are derived from amino acide 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Aaw91262 Apolipopr Aaw96826 Amino acil Aau98981 Human apol Ad46777 Human Pro Abr40253 Human ali Abr40253 Human ali Abr40253 Human ali Abr40391 Human apol Adh18871 Human apol Adh18870 Human apol Adh18870 Human apol Ado33445 Human apol Adu33184 Novel human apol Aau33184 Novel human apol Aau3130 Human apol Aau3130 Human apol	000010
AAW41262 AAW96826 AAW9681 AAU9881 AAO15893 AAO15893 ABR40253 ABR40253 ABR40253 ABR43408 ADH18871 ADH18871 ADH38870 ADH38870 ADH38870 ADH3871 AAU21930 AAU21930	AAE10805 ADA89379 ADA89383 ADA89391 ADA89389
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ALIGNMENTS

RESULT 1

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Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                             Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                          Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                                                                                                                                                                                                                   Claim 17; Page 58; 70pp; English.
      AAY30700 standard; peptide; 11
                                                                                                                                                                                         98US-0077618P.
                                                                                                                                                                      99WO-US004805.
                                                                                                                                                                                                                            Innerarity TL, Boren JOS;
                                          (first entry)
                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                              WPI; 1999-551509/46.
                                                                                                       Synthetic.
Homo sapiens.
                                                                                                                                   WO9946598-A1.
                                                                                                                                                                     05-MAR-1999;
                                                                                                                                                                                        10-MAR-1998;
                                         17-NOV-1999
                                                                                                                                                    16-SEP-1999.
                         AAY30700;
AAY30700
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Gaps

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Score 51; DB 2; Length LL, Pred. No. 0.0043;

92.7%;

1; Mismatches

10; Conservative

Query Match Best Local Similarity Matches 10; Conserv

Sequence 11 AA;

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TRLTRKDRGLK 11

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11

1 TRLTRKERGLK

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AAY30582-Y30700 represent apo-BL100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atherosaclerosis. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to revent the formation of atherosclerotic lesions and prevent can be used to prevent the formation of atherosclerotic lesions and prevent can an apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a therosclerotic regions. Thus the assays may be used to determine whether compounds windlar atherosclerotic regions. Thus the assays may be used to determine whether compounds condition of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerotic lesions are mammal
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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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100.0%; Pred. No. 0.0007;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                         Sequence 11 AA;
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Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation.

Homo sapiens. WO9946598-A1

Synthetic

99WO-US004805

05-MAR-1999; 10-MAR-1998;

16-SEP-1999

Innerarity TL, Boren JOS;

WPI; 1999-551509/46.

(REGC) UNIV CALIFORNIA.

AAY30697 standard; peptide; 11 AA.

RESULT 3 AAY30697

(first entry)

17-NOV-1999

AAY30697;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which creeptor mutations. They were created to identify compounds which compounds which after mainto acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and manmals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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Pred. No. 0.1;
1; Mismatches
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Best Local Similarity
Matches 9; Conservat
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1 TRLTRKDRGLK 11

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AAY30699;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the atherosclerosis, and in vivo assay methods for identifying also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                                                                         Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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Matches 10, Conservative
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                                                                                                                                                                                                                                                Synthetic.
                              AAY30683;
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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Pred. No. 0.26;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
1 TRLTREKRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRKDRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLTRDKRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
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Gaps

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RESULT 5 AAY30683 £

ð 유 Zyskind JW; Xu HH;

ξĘ

Ohlsen Forsyth

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P
08-FEB-2002; 2002US-000750
06-MAR-2002; 2002US-036269951
                21-MAR-2002; 2002WO-US009107
                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                           WPI; 2003-029926/02.
                                                                                                                                                                                                       N-PSDB; ACA28420
                                          21-MAR-2001;
                                                                                                                                                     Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                 AAY30582-Y30700 represent apo-BL00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which and added are derived from anino acids 3358 conditions are derived from anino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method computed which disrupt LDL-PG binding with broteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which express human apo-BL00 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                              identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gарв
Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.8%; Score 39.5; DB 2; Length 10; 90.9%; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #10077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU24550 standard; protein; 621 AA.
                                                                                                                                                                                                                                                                                                                           Claim 17; Page 57; 70pp; English.
                                                                                                                                                              98US-0077618P.
                                                                                                                                     99WO-US004805
                                                                                                                                                                                                                     Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRKD-GLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRKDRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium botulinum.
                                                                                                                                                                                                                                               WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                      Homo sapiens.
                                                                                                                                                              10-MAR-1998;
                                                                              WO9946598-A1
                                                                                                                                    05-MAR-1999;
                                                                                                          16-SEP-1999
                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU24550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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the 6113 antisense sequences given in the specification where expression of the 612 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a call. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antiense concluding a polypeptide whose expression is inhibited by the antiense concluding the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or proliferation or that inhibits cellular proliferation; (8) required for poliferation, or that inhibits cellular proliferation of an organism the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overaxpressed of underexpressed; (12) determining the extent to proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for cellular proliferation in cells other than S. aurens, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 6; Pred. No. 68; 2; Mismatches
                                                                                                                                                           Claim 25; SEQ ID NO 52474; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN47108
ID ADN47108 standard; protein; 1756 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.0-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLTRKDRGL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 621 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SXXXE
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WO200277183-A2.

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LDL; receptor component; apo B100 receptor site.
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  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential date of the genome of such organism, selecting at least I arbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly armococcus kodakaraensis KOD1. The method is for targeting the thermococcus kodakaraensis KOD1. The method is for targeting the studying gene structure and functions as well as enzyme activities of studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the chooled by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                             Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                  gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1756;
          Thermococcus kodakaraensis KOD1 protein sequence SeqID986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 8;
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 986; 598pp; Japanese.
                                                                                                                                                                                                                                 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                29-AUG-2003; 2003WO-IB003597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo B binding site peptide 2.
                                                                                                                                                                                                        30-AUG-2002; 2002JP-00319011.
                                                                                                    Thermococcus kodakaraensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTRKDRGL 10
                                                                                                                                                                                                                                                          Imanaka T, Atomi H;
                                                                                                                                                                                                                                                                                     WPI; 2004-257583/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1756 AA;
                                                                                                                             WO2004022736-A1.
                                                                                                                                                       18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57205;
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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDD) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 ipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEVKKNKHRH (1) or TTRITKKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 52; 73pp; English.
                                                                                                                                                                                                                                                                                  96GB-00020153.
                                                                                                                                                                                                             97WO-GB002610.
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                                                                                                                                                                                                                                                                                                                                               (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRKDRGLK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                           Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                    WO9813385-A2
                                                                                                                                                                                                             25-SEP-1997;
                                                                                                                                                                                                                                                                                  27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1998
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                                                                                                                                         02-APR-1998
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57207;
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This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprosein B-100 (apoB-100). 21-KAQ-XX-KACKHKHS-XZ-T-ZZ (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (a3); Z2 = the C terminus of the peptide, or 1-47 amino acids or Compositions containing the peptide, are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromopplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. curing or after surgery or in cases of heart attack stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits activation of the prothrombinase complex; and prevents activation of cativation of thromopolastin. Since (I) are much smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollpoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                        Peptide fragments of apo:lipo:protein B-100 with anticoagulant activilused for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%; Score 38.5; DB 2; Length 15; 90.9%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.7;
0; Mismatches
                                                                                                                                                                                     Disclosure, Page 22; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW96892 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00874807.
  Bruckdorfer KR, Ettelaie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRKDRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRK-RGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoogeveen
                                                WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW96892
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKNKHRH (1) or TTRLTRREGER (2), or that cinvention are peptides containing, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.5; DB 2; Length 13; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                   Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 7; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B-100 fragment,
                                            97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%;
                                                                                        96GB-00020153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                    (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||
TRLTRK-RGLK 12
                                                                                                                                                                                 Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRKDRGLK 11
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                                                                                                                                                                                                                           WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 AA;
                                                                                        27-SEP-1996;
                                                                                                                                                                            Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9743311-A1
02-APR-1998
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Length 20;

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Score 38.5; DB Pred. No. 2.4;

70.0%;

Sequence 20 AA;

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                                                                                                     AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to cukaryotic cells, in vivo or in vitro, for expressing a therapoutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.5; DB 2; Length 15; Pred. No. 1.7; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin binding peptide sequence #28.
                                                        Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001US-0306726P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.0%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRKDRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TRLTRK-RGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ETHZ-) ETH ZUERICH (UYZU-) UNIV ZURICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
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     treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10 montion are peptides containing an apo B binding sequence with at least of montity with sequences: KAEYKKNKHRH (1) or TRETRERGIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                                                                                                                Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                   Gaps
                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                 Indels
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                                                                                                                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "attached to retinoic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "attached to cholesterol"
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Pred. No. 2.6;
                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                 AAW57208 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB002610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that express this receptor.
                                                                                                                                                                                                                                                                (first entry)
                                                 Conservative
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                                                                                                         7 TRLTRK-RGLK 16
                                                                                  1 TRLTRKDRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owens MD,
Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                   AAW57208;
                                                                                                                                                                   RESULT 14
                                                                                                                                                                                    AAW57208
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Search completed: January 13, 2005, 01:43:05 Job time : 86.1011 secs

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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a nonnaturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least of the actually occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete appearance, which is large and tends to aggregate, to provide binding
   1;
                                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
 Gaps
   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 38.5; DB 2; Length 22; 90.9%; Pred. No. 2.6; ive 0; Mismatches 0; Indels
   0; Indels
                                                                                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "attached to retinoic acid"
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apo B sequence, which is larye מוט נכּ
affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                             AAW57209 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baillie G;
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96GB-00020153.
                                                                                                                                                                                                            03-AUG-1998 (first entry)
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.9
Matches 10; Conservative
                                TRLTRKDRGLK 11
                                                      7 TRLTRK-RGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halbert GW,
                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                             RESULT 15
AAW57209
Matchee
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Gaps

1;

TRLTRKDRGLK 11 TRLTRK-RGLK 16

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 13, 2005, 01:30:05; Search time 15.8689 Seconds (without alignments) 66.696 Million cell updates/sec Run on:

US-09-823-418-19 55 1 TRLTRKDRGLK 11 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		ъ	apolipoprotein B -	apolipoprotein B-1	ď	hypothetical prote			hypothetical prote	apolipoprotein B-1	apolipoprotein B -	hypothetical prote		16S rRNA 5'-region	transposase, IS605	conserved hypothet		probable invasion	glucosyltransferas	hypothetical prote	C-terminal domain					hypothetical prote	늄	
SUMMARIES	ΩI	D98082	BWASBE	AC1031	832802	LPHUB	F95218	E81098	AI2432	A37842	AE1987	C60950	JH0102	F71164	873019	D64337	C72305	A81651	E91092	A85938	T49903	F96624	C97177	H84008	AI2112	T01531	NKVLHH	AC1148	AD0722	G84799
	DB	7	Н	N	~	Н	~	N	N	~	N	~	N	N	N	N	~	N	N	~	~	N	N	N	7	N	-	7	0	0
dip	Query Match Length	250	2073	807	596	4563	250	78	236	321	384	269	779	195	331	389	405	419	458	458	488	543	246	248	264	289	305	341	389	419
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hypothetical prote hypothetical prote	probable alpha-amy dermonecrotic toxi	364K Golgi complex apolipoprotein B-1	urease (EC 3.5.1.5	hypothetical prote	ct386 hypothetical CT386 hypothetical	probable binding p	conserved nypothet hypothetical 36.8K	hypothetical prote	hypothetical prote
H71491 H86146	E96720 I40325	JC5837 E60950	A36950 B85356	869732	H72071 E86551	D83010	A81597 JQ0855	S49963	840752
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33	33	33 32.5	3 3	35	3 3 3 3 3 3	32	3 2	32	32
30 31	33 33	34 35	36	38	e 4 e 0	4,	4 4 2 6	44	45

ALIGNMENTS

D98082
Cipecial protein fecE [imported] - Streptococcus pneumoniae (strain R6)
Cipecial protein fecE [imported] - Streptococcus pneumoniae
Cipecias Streptococcus pneumoniae
Cipecias Streptococcus pneumoniae
Cipecias Streptococcus pneumoniae
Cipaces 32-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cipaces 10-10 198082
Rihoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
S.; R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Barteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Areference number: A97872; MUID:21429245; PMID:11544234
A; Accession: D98082
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT:Q8DNJ3; GB:AE007317; PIDN:AAL00489.1; PID:g15459361; GSPDB

A;Gene: fecE C;Superfamily: inner membrane protein malK; ATP-binding cassette homology

Gaps ö 72.7%; Score 40; DB 2; Length 250; 70.0%; Pred. No. 2.8; cive 3; Mismatches 0; Indels Best Local Similarity 70.0 Matches 7; Conservative Query Match

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1 TRLTRKDRGL 10 :|||:||||: 47 SRLTKKDRGV 56 g ò

Different - Emericella nidulans C;Species: Emericella nidulans Aspergillus nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Species: Emericella nidulans, Aspergillus nidulans a3.1-Dec-1991 #text_change 09-Jul-2004 C;Accession: A37879 B;Engle, D.B.; Osmani, S.A.; Osmani, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R. A;Engle, D.B.; Osmani, S.A.; Osmani, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R. A;Title: A negative regulator of mitosis in Aspergillus is a putative membrane-spanning A;Accession: A37879 A;Molecule type: mRNA A;Accession: Administration to three predated transmembrane domains, there are several potent: asein kinase, and one sequence that resembles a nuclear localization signal C;Comment: This protein is part of a regulatory pathway that includes the nimA protein term mitosis and prevent them from leaving mitosis.

A, Gene: bimE C, Superfamily: bimE protein

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Ajaccesion: A225, Ashocesion: A2541-3823, 'R', 3825-4563 <CLA>
Ajaccesion: A2549, 'S', 2541-3823, 'R', 3825-4563 <CLA>
Ajaccesion: A2263

Ajaccesion: A2263

Ajaccesion: A2263

Ajaccesion: A2263

Ajaccesion: A2263

Ajaccesion: A2263

Ajaccesion: A2264

Ajaccesion: A2264

Ajaccesion: A2264

Ajaccesion: A2264

Ajaccesion: A2265

Ajaccesion: A2266, NUD: 87016385; PMID: 3763409

Ajaccesion: A2264

Ajaccesion: A2266

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                                         N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A2452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-617, A', 619-1929, 'F', 1931-3318,'D', 3320-3426,'T',3428-3431,'Q',3433-3731,
A;Residues: 1-617,'A', 619-1929, 'F', 1931-3318,'D', 3320-3426,'T',3428-3431,'Q',3433-3731,
A;Cross-references: UNIPROT: P04114; UNIPROT: P78492; UNIPROT: P78479; UNIPROT: QOUMNO; UNI
B;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
B;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A;Reference number: A91058; MUID:87161758; PMID:3030729
                                                                                                                                                                                                                                                                                                                                    A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Accession: A27850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein STV4573 [imported] - Salmonella enterica subsp. enterica serovar Typi, Species: Salmonella enterica subsp. enterica serovar Typhi () Species: Salmonella enterica subsp. enterica serovar Typhi () Decies has also been called Salmonella typhi () Decies has also been called Salmonel, Ext. Change 18-Nov-2002 () Are thin, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L., T.; Connerton, P.; Cronin, A.; Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. () Antherism S.; O'Gaora, P. () Antherism Salmonella enterica serovalitie: Complete genome sequence of a multiple drug resistant Salmonella enterica serovalities complete senome sequence of a multiple drug resistant Salmonella enterica serovalities complete senome sequence of P. () PMID:11677608
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C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Accession: 332802
E;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynoniqus monkey: evidence for post-transcriptional re A;Reference number: 532802; MUD: 92075708; PMID: 1742325
A;Accession: 832802
A;Accession: 832802
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-59 c PAP>
A;Cross-references: UNIPROT: Q28473; EMBL: X15737; NID: 938047; PIDN: CAA33755.1; PID: 993012
C;Superfamily: apolipoprotein B
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                                                                                                                                                                                                                Length 2073;
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C;Keywords: cell cycle control; mitosis; transmembrane pro
$1,162-1643/Domain: transmembrane #status predicted <TMl>-
F;168-1703/Domain: transmembrane #status predicted <TM2>-
F;1746-1764/Domain: transmembrane #status predicted <TM2>
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Pred. No. 14;
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0; Mismatches
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Pred. No.
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80.0%;
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88.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                       8; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-807 <PAR>
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Best Local Similarity
Matches 8; Conserv
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C;Genetics:
A;Gene: STY4573
                                                                                                                                                                                                                                                                                       Matches
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LPHUB
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A; Residues: 1-97, 1', 99-128, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428 A; Residues: 1-97, 'I', 99-128, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428 A; Residues: 1-97, 'I', 99-128, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428 A; Cross-references: GB:J02610; NID:G1RB03; PIDN:AAA35549.1; PID:G178804 A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptide: R; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptide: R; Note: Nail, Acad. Sci. U.S.A. 83, 5678-5682, 1986 A; Ttle: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein A; Reference number: A24320; MUID:86287319; PMID:3461454 A; PIGRIPNCFSNGLICYSLWLHSFQ: A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138,' PTGRLPNCFSNGLICYSLWLHSFQ: A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138,' PTGRLPNCFSNGLICYSLWLHSFQ: A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138,' PTGRLPNCFSNGLICYSLWLHSFQ: A; Law, S.W., Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985 A; Ttle: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A; Reference number: A24684; MUID:86094221; PMID:3001697
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A, Residues: 485-617, A', 619-1044 <LA2>
A, Residues: 485-617, A', 619-1044 <LA2>
A, Cross-references: 488-M12480; NID: 9178791; PIDN: AAA51751.1; PID: 9178792
A, Cross-references: GB: M12480; NID: 9178791; Miller, J.; Appleby, V.; Chen, G.C.; K
R, Procter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; K
P. Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A, Reference number: A94088; MUID: 86149325; PMID: 3513177
A, Rocestion: A23817
A, Residues: 1-291 <RRO>
A, Residues: 1-291 <RRO>
A, Cross-references: GB: M12681; NID: 917877; PIDN: AAA51753.1; PID: 9178798
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Ajaccession: A24269
Ajmolecule type: mRNA
Ajmolecule type: protein
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A;Reference number: A22006, MUID:84208786; PMID:6373369
A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-892, K',894-896 <LEI>A;Residues: 873-892, K',894-896 <LEI>A;Residues: 813-892, K',894-896 <LEI
A;Residues: 813-892, K',894-896 <LEI
A;Residues: 813-892, K',894-896 <LEI
A;Residues: 814-892, K',894-896 <LEI
A;Title: Structure of the human apolipoprotein B 100 gene.
A;Reference number: A99715; MUID:87271140; PMID:2866136
A;Contents: annotation; gene structure
A;Reference number: A99715; MUID:87271140; PMID:2866136
A;Title: Human apolipoprotein B-100 heparin-binding sites.
A;Reference number: A99715; MUID:8780197; PMID:3301850
A;Title: Human apolipoprotein B-100 heparin-binding protein.
A;Reference number: A98268; MUID:8780197; PMID:308780
A;Title: Apolipoprotein B-18 a calcium binding protein.
A;Reference number: A9015; MUID:862422445; PMID:3087360
A;Contents: annotation; heparin binding protein.
A;Reference number: A9015; MUID:86422445; PMID:3087360
A;Contents: annotation; heparin binding protein.
A;Reference number: A9015; MUID:86422445; PMID:3087360
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R; Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell,
Nucleic Acids Res. 13, 8813-8826, 1985
A; Title: Molecular cloning of human apolipoprotein B cDNA.
A; Reference number: 137178; MUID:86093680; PMID:3841204
A; Accession: 137180
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              A;Reference number: A24269; MUID:86041888; PMID:3903660
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Pred. No. 98;
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A; Residues: 1671-2323, 'PYW', 2327-2352,'H', 2354-2398 <HAR>
A; Residues: 1671-2323, 'PYW', 2327-2352,'H', 2354-2398 <HAR>
A; Cross-references: GB:M17367; NID:g178731; PIDN:AAA51741.1; PID:g178732
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A; Therosclerosis SB: 277-289, 1985
A; Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on A; Reference number: A90084; MUID:86130855; PMID:3841481
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A;Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55
36;1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
A;Note: these fragments were derived from apo48
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A;Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism p
A;Reference number: A28002; MUID:88106542; PMID:3426612
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A;Residues: 1282-2721,2722-3290,'L',33292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A;Cresidues: 1282-2721,2721-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A;Cresidues: 1282-2721,2721; NID:9178817; PIDN:AAA51758.1; PID:9178818
R;Hardman, D.A.; Profter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
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A;Title: Structural comparison of human apolipoproteins B-48 and B-100.
A;Reference number: A29671; MUID:88050832; PMID:3676265
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A, Residues: 'N', 3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3365-3982,'S', 33

A, Cross-references: GB:M12413; NID:gJ78735, PIDN:AAA51742.1; PID:g178736

R, Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai

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A, Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in

A, Reference number: A40133; MUID:88018019; PMID:3659919
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A; Residues: 4219-4337,'S',4339-4563 <PFI>
A; Cross-references: GB: M36676
R; Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.
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A; Reference number: A24738; MUID: 86042646; PMID: 2932736
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A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete structure of the B-74
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A; Residues: 2165-2179 cCH1>
A; Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A; Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
A; Accession: A40133
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A,Rebidues: 709-791, SSSWKAASHGCPHSAGD', 810-906 <DEE>
A,Cross-references: GB:K03175, NID:g178821; PIDN:AAA51759.1; PID:g178822
R,Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
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A;Title: Analysis of the human apolipoprotein B gene; complete structure
A;Reference number: A91565; MUID:87191999; PMID:2883086
R;Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
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A;Title: A paraial cDNA clone for human apoliprotein B.
A;Reference number: A25774; MUID:85270450; PMID:3860836
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A;Residues: 3846-4298 <SHO>
K;Pfitzner, R.; Wagener, R.; Stoffel, W.
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A;Title: Isolation, expression and characterization of a
A;Reference number: A25572; MUID:87076044; PMID:3024665
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A;Residues: 2129-2179,2181-2235 <HA2>
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Fixeneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,: DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A/Reference number: AB1807; MUID:21595285; PMID:11759840

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A/Accession: AF1040

A/Accession: AF1040

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A;Cross-references: UNIPROT:P29978; GB:BA000019; PIDN:BAB73405.1; PID:g17130795; GSPDB:
A;Experimental source: strain PCC 7120
                                     A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-236 <KUR>
A,Residues: 1-236 <KUR>
A,Ecseridues: UNIPROT:Q8YMB7; GB:BA000019; PIDN:BAB76716.1; PID:g17134155; GSPDB: A,Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Anabaena sp.
C;Date: 21-Jun-1991 #sequence_revision 21-Jun-1991 #text_change 09-Jul-2004
C;Accession: A37842
E;Ammers, P.J.; McLaughlin, S.; Papin, S.; Trujillo-Provencio, C.; Ryncarz II, A.J.
J. Bacteriol. 172, 6981-6990, 1990
A;Title: Developmental rearrangement of cyanobacterial nif genes: nucleotide sequence, A;Reference number: A37842; MUID:91072249; PMID:2123860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 1 (xisA 3' region) - Anabaena sp. (strain PCC 7120)
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A Modecule type: DNA
A Modecule type: DNA
A Residues: 1-321 clam>
A Cross-references: UNIPROT: P29978; GB: M38044
C; Superfamily: Anabaena hypothetical protein 1 (xisA 3' region)
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
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C;Superfamily: Anabaena hypothetical protein 1 (xisA 3' region)
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1
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Pred. No. 27;
1; Mismatches
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llarity 87.5%; Pred. No. 43;
Conservative 0; Mismatches
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Pred. No. 36;
0; Mismatches
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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152 RLKRKDRG 159
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Best Local Similarity
7; Conserve
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Acteslan, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Attle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: F95218

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A.Note: Nostoc sp. strain PCC 7120
Cispecies: Nostoc sp. strain PCC 7120
Ciscossion: A12432
Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S N. Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anales Reference number: AB1807; MUD:21595285; PMID:11759840
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C, Genetics:
A, Gene: SP1871
C, Superfamily: inner membrane protein malk, ATP-binding cassette homology
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Pred. No. 18;
4; Mismatches 0; Indels
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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A;Accession: F71164
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Actus: preliminary;
A;Gatus: preliminary;
A;Residues: 1-195 cKAW>
A;Residues: 1-195 cKAW>
A;Cross-references: UNIPROT:O58251; GB:AP000002; NID:G3236129; PIDN:BAA29603.1; PID:g32
A;Cross-references: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             daunorubicin resistance protein drrA - Mycobacterium leprae
daunorubicin resistance protein
C; Species: Mycobacterium leprae
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C; Accession: $73019
R; Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid L518.
A; Reference number: $72591
A; Reference number: $73019
A; Reference number: $73019
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-331 < SMI>A; Residues: UNIPROT: Q49938; EMBL: U00023; NID: 9467194; PIDN: AAA17362.1; PID: 9467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Methanococcus januaschii.
C;Species: Methanococcus januaschii.
C;Species: Methanococcus januaschii.
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence 0.3.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.S.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch, A;Accession: D64337
A;Reference mumber: A64300; MUID:96337999; PMID:8688087
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-389 <BULD.
A;Cross-references: UNIPROT:Q57747; GB:U67485; GB:L77117; NID:g1591020; PIDN:AAB98286.1
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                                                                                                                                                                                                                                                                                                                                                         Length 195
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
A; Reference number: A71000; MUID: 98344137; PMID: 9679194
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C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;25-216/Domain: ATP-binding cassette homology <ABC>
F;42-49/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                         2;
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Pred. No. 35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                      61.8%;
60.0%;
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A,Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 RCSEKDRGIK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLTRKDRGLK 11
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58 LTRPDRGL 65
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D64337
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submitted to GenBank, June 1990
submitted to GenBank, June 1990
A;Refearce number: A38864
A;Accession: JH0102
A;Molecule type: DNA
A;Residues: 1-779 <SMI>
A;Residues: 1-779 <SMI>
A;Residues: 1-779 <SMI>
A;Residues: 1-779 <SMI
A;Mote: this is a revision to the sequence from reference JH0101
B;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of ap A;Reference number: JH0101; MUID:90236327; PMID:2332175
A;Contents: annotation
                                                                                                                                                                                                               Ritaw, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
J. Kritler. A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A; Reference number: A60950; MUID:90324804; PMID:2373961
A; Rocession: C60950
A; Rocession: Logo Comparison
A; Ross-references: UNIPROT:060537; UNIPROT:060536
C; Superfamily: apolipoprotein B
C; Superfamily: apolipoprotein B
C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: F71164
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
P;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                     C;Spelies: Mesocricetus auratus (golden hamater)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein B - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.5; DB 2;
Pred. No. 38;
1; Mismatches 0;
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Pred. No. 1.1e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PH0515 - Pyrococcus horikoshii
                                                                                                 apolipoprotein B-100 - golden hamster (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.7%;
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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642 SRLTRK-RGLK 651
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Query Match 61.8%; Score 34; DB 2; Length 389; Best Local Similarity 85.7%; Pred. No. 69; Matches 6; Conservative 1; Mismatches 0; Indels
C, Superfamily: fructose-1,6-bisphosphatase, archaeal type
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0; Gaps

3 LTRKDRG 9 :|||||| 380 ITRKDRG 386 Op

Search completed: January 13, 2005, 01:52:43 Job time : 16.8689 secs

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1 TRLTRKDRGL 10
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Best Local Similarity
7; Conserve
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47 SRLTKKDRGV
                                                                                                                                          Q8DNJ3
                                                                                                                             RESULT 1
OBDNJ3
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                                                                                                                                                                                                                                                                                                                      0794r5 actus vocif
01378 home sapien
01378 home sapien
07260 home sapien
072595 leptospira
08668 leptospira
Aas70931 leptospira
0807711 photochabdu
                                                                                                                                                                                                                                                                                                                                                                                                                               O7ps51 anopheles g
O8gla1 streptococc
O6ndr2 rhodopseudo
Cae25486 rhodopseu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6nv26 brachydanio
Q8jhj0 brachydanio
Aah68340 brachydan
                                                                                                                                                                                                                                                                                                           mus musculu
salmonella
                                                                                                                                                                                                                                                                                                                                                                                                          Aad22478 lactobaci
Q97ny0 streptococc
Q9ulc0 homo sapien
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Aap68309 arabidops
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                                                                                                                                                                                                                                                                                                                                                                                                     P26931 lactobacill
                                                                                                                                                                                                                                                                                                    emericella
                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                (without alignments)
73.735 Million cell updates/sec
                                        January 13, 2005, 01:15:45; Search time 85.8361 Seconds
5.1.6
Compugen Ltd
                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                     1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                          SUMMARIES
GenCore version (c) 1993 - 2005
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URE3_LACFE
AAD22478
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GSHR ARATH
AAM98183
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BIME EMENI
Q99JK2
Q8Z1J2
Q7YQRS
Q28473
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EMCN HUMAN
Q7PS51
                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                           - protein search, using sw model
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AAP68309
QGNV26
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AAH68340
Q8RWG0
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Gapop 10.0 , Gapext 0.5
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Q6NDR2
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                    US-09-823-418-19
55
                                                                                  1 TRLTRKDRGLK 11
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Match Length DB
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100
250
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283
370
370
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Maximum DB
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                                                                                   Sequence:
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                                         Run on:
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Glass J.I.;

Glass J.I.;

Glass J.I.;

Tennome of the bacterium Streptococcus pneumoniae strain R6.";

R. J. Bacteriol. 183:5709-5717(2001).

C. I. SIMILARITY: Belongs to the ABC transporter family.

ENBL; AB00882; D98082.

B.R. J. Bacteriol. 1970.

B.R. J. Bacteriol. 1070.

C. Go.0006020; C. Membrane; IEA.

GO; GO.000060524; F.ATP-binding, IEA.

GO; GO:0000166; F.ATP-binding, IEA.

GO; GO:0006166; F.ATP-binding, IEA.

GO; GO:0006109; F.ATP-binding; IEA.

GO; GO:0006109; F.ATP-binding, IEA.

InterPro; IPR003533; AAA ATPRASS.

InterPro; IPR003533; AAA ATPRASS.

InterPro; IPR003533; AAA ATPRASS.

InterPro; IPR003653; ABC_transporter.

PRODOM: P0000006; ABC_transporter; I.

PRODOM: P0000006; ABC transporter; I.

SWART; SM00382; AAA; I.
                             Q88ul5 encephalito
Q8divO synechococo
Q8ymb7 anabeana sp
Q8typ9 actinobacil
Q8kivJ pseudomonas
P29978 anabaena sp
Q8fie corynebacte
Q9h834 homo sapien
G27C0 oryza sativ
Bad07650 oryza sat
neisseria m
                    caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC BAA-255 / R6;
STRAIN=ATCC BAA-255 / R6;
STRAIN=210-245; PubMed=11544234;
MBDLINN=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
Glass J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-ferric iron transport.
Name=fecE; OrderedLocusNames=spr1686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PSSO893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_toccome.
SEQUENCE 250 AA; 28528 MW; FFC841A29F30033D CRC64;
                                                                                                                                                                                                                                                                                                                                                                           250 AA
                                                                                                                                                                                                                                                                                    ALIGNMENTS
              Q95X71
Q8SUL5
Q8DLVO
Q8YMB7
Q84 0G9
Q8KIP9
Q8KIV1
YE48 ANASP
                                                                                                                                                                         О9Н834
О627С0
ВАD07650
ВАD07928
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                   00000000000
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NCBI_TaxID=171101;
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Gaps

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72.7%; Score 40; DB 2; Length 250; 70.0%; Pred. No. 7.2; 1.2; ive 3; Mismatches 0; Indels

Conservative

56

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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XX Tatabberg R.L., Faingold B.A., Grouse L.H., Darge J.G.,

Straubberg R.L., Faingold B.A., Grouse L.H., Darge J.G.,

X Alausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phokins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahasley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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MEDLINE21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE21534947; PubMed=1.5. James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Cronin A., Davies R.M., Dowles R.M., Davies R.M., Davies R.M., Davies R.M., Then T.T., Holroyd S., Jagels K., Fellwell T., Hamin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Waltehead S., Mannella Rutterland S., Call Rutterland S., Call Rutterland S., Call Rutterland S., Mannella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Length 438; Pred. No. 23; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MF-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC006060, AAH06660.1; -.
MGD; MGI:1913808; Lars.
InterPro; IPR002088; PPTA,
InterPro; IPR00900; LRASyn la_bind.
PROSITE; PS00904; PPTA; UNKNYM 1.
SEQUENCE 438 AA; 49840 MM; ZE730A99D65AFRFO CPCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8Z1J2; Q7C5G1;
QH-MRA-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=STY4573, t4270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein STY4573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 RLTKTDRGIK 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Czech II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8Z1J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
Q8Z1J2
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOCC OCT TO THE SECOND THE SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; JPR002015; APC proteasome.
Pfam; PF01851; PC_rep; 4.
Mitosis; Repeat; Transmembrane.
DOMAIN 342 353 Nuclear localization signal (Potential).
TRANSMEM 1623 Potential.
TRANSMEM 1685 1703 Potential.
TRANSMEM 1746 1764 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE=90375468; PubMed=1697851;
Engle D.B., Osmani S.A., Osmani A.H., Rosborough S., Xiang X.,
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella.
NCBI_TaxID=162425,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A negative regulator of mitosis in Aspergillus is a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 2073;
Pred. No. 88;
1; Mismatches 1; Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                  2073 A.A.
                                                                                                                                                                                                                                                                                                                                       Emericella nidulans (Aspergillus nidulans)
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229178 MW;
                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                         Negative regulator of mitosis.
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80.0%;
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                               STANDARD;
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                                                                                                                                                                   01-MAR-1992 (Rel. 21, 01-MAR-1992 (Rel. 21, 05-JUL-2004 (Rel. 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1746 176
2073 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morris N.R.;
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01-JUN-2001 (
01-JUN-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A37879
                                                                                                               BIME EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
SEQUENCE
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                                                                                                                                      P24686;
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                                                                           BIME_EMENI
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Matches
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                                                 RESULT
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PRT; 4563 AA.
P04I14; 000502; Q13787;
01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structure
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               MEDLINE=9205708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
Mapo B metabolism in the cynomolgus monkey: evidence for post-
transcriptional regulation.";
Biochim. Blophys. Acta 1086:326-334(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 38.5; DB 2; Length 3262; 90.9%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                  Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; XIS737; CAA33755.1; -.
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete
                                                                                                                                                                                                                                                                                                                                                                                                                                   66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the B-74 region..;
Gene 49:29-51(1986).
BMBL; MI5421, AAA51758.1; -.
BMRL; MI5421, AAA51758.1; -.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005519; F:lipid transporter activity; NAS.
NON_TER.
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Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.9'
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 TRLTRK-RGLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                        596
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596
596 AA;
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                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                            Lipoprotein.
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01-JUN-2003
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NON TER
SEQUENCE
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APB_HUMAN
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                                       STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=225313767; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
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Actus vociferans (Spix's owl monkey).
Actus vociferans (Spix's owl monkey).
Mexaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
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MEDLINE=22761261; PubMed=12878460;

Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Apolloportein B (Fragment)
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae;
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EMBL, AE016848; AAO71728.1; -.
COMDLETE PROCESSED HYPOCHERICAL PROCESSED SEQUENCE 807 AA; 90698 MW; 577CIDA31611BCF0 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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88.9%; Pred. No. 47;
iive 0; Mismatches
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NCBI_TaxID=9541;
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VARIANT SER-4338.
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     "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
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Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
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MEDLINE-87068468; PubMed=3759943;
Gohn S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
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MEDLINE=86041888; PubMed=3903660;
Mentabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
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Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete CDNA and derived protein sequence of human apolipoprotein
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MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
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derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleogtomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.,
"DNA sequence of the human apolipoprotein B gene.";
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Zannis V.I.;
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MEDLINE-85270450; Pubmed=3860836;
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"A partial cDNA clone for human apolipoprotein B."
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                           Homo sapiens (Human).
                                                                                        SEQUENCE FROM N.A.
  (Apo B-48)].
                                                               NCBI_TaxID=9606;
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SEQUENCE OF 1-291 FROM N.A.
MEDLINE=86149325; PubMed=3913177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
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MEDLINE=88018019; PubMed=365919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
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Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.;
Cunny G., Cambien F., Roizes G.;
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MEDLINE=89098975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
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MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
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Mol. Biol. Cell 11:721-734(2000)
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-FUNCTION: Apollopprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
                                                                                                                                      VARIANT FDB CYS-3558.
MEDLINE=95190020; PubMed=7883971;
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mutation that decreases LDL receptor binding affinity.";
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AND ILE-3921.
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Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.,
"Detection of new variants in the apolipoprotein B (Apo B) gene by
                                                                 MEDLINE=91016974; PubMed=2216805;
Huang L.-S., Gavish D., Breslow J.L.;
"Sequence polymorphism in the human apoB gene at position 8344.";
Nucleic Acids Res. 18:5922-5922(1990).
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Karyota; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 4563 AA
                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS FDB GLN-3527 AND CYS-3558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                              MEDLINE=97044521; PubMed=8889592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98141125; PubMed=9490296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                      Hum. Mutat. 8:282-285(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Wascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
A PubMedel5028702;
A Mascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
A P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
A Marques M.V. Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
A Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.T.,
Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA Jeronimo S.M., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA Gondarative genomics of two Leptospira interrogans serovars reveals
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT "Dovel insights into physiology and pathogenesis.";
I Bacteriol 186:2164-2172(2004).
BRIEL, AE017286; AAST0911.1;
BRIELP, RED12286; MAST0911.1;
BRIELP, RED12286; MAST0911.1;
BRIELP, RED12286; MAST0911.1;
BRIELP, RED12286; MAST0911.1;
BRIELP, RED12080; MAST0911.1;
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NCBI_TaxID=44275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
Copenhageni).
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0
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Pred. No. 4.7e+02;
0; Mismatches 0; Indels 1;
Rieder M.J., Carrington D.P., da Ponte S.H., Haetings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX324608; AAP72970.1; -..
GO; GO:0005519; F:lipid transporter activity; IEA.
InterPro; IPR00144; DUF1081.
InterPro; IPR00144; Lipid transport; IEA.
Fig. P. P. Lipid transport; IEA.
Fig. P. Lipid transport; IEA.
Fig. Co. GO:0006669; Pilpid transport; IEA.
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Pred. No. 26;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
3-methyladenine DNA glycosylase.
Name=alkA; OrderedLocusNames=LIC12362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA
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                                                                                                                                                                                                                                                                                                                  Pfam; PF06448; DUF1081; 1.
Pfam; PF01347; Vitellogenin N; 1.
SMART; SM00638; LPD N; 1.
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90.9%;
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SMART; SM00478; ENDO3c; 1
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7; Conservative
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STRAIN=Fiocruz L1-130;
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ses 10; Conserv
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Best Local S
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RESULT 11

[1] SEQUENCE FROM N.A. NCBI_TaxID=9606;

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Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.; "Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis."; J. Bacteriol. 186:2164-2177(2004).

EMBL, AE017296; AAS70931.1; -. SEQUENCE 213 AA, 24639 MW; 73E6CA3E0C737487 CRC64;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=15188426; Gilnblat M., Hikasa H., Sokol S.Y., Grinblat Y., Gilnbouse M., Wagner Nyholm M., Hikasa H., Sokol S.Y., Grinblat Y., "Two Frodo/Dapper homologs are expressed in the developing brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to unknown protein.
OrderedLocusNames=plu1085;
Photorhabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriais Enterobacteriais.
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MEDLINE=21984492; Pubmed=11941372;
Gloy J., Hikasa H., Sokol S.Y.;
"Frodo interacts with Dishevelled to transduce Wnt signals.";
Nat. Cell Biol. 4:351-357(2002).
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                                                                                                                                                                                                                          Score 37; DB 2; Length 213;
Pred. No. 26;
2; Mismatches 0; Indels
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Hikasa H., Sokol S.Y.;
EMBL; AY208659; AA049711.2; -.
ZEIN; ZDB-GENE-030131-9975; dact.
SEQUENCE 838 AA; 91349 MW; 6906BSECC35012BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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72.7%; Pred. No. 1.3e+02;
iive 1; Mismatches 2;
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                                                                                                                                                                                                                                67.3%;
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Dev. Dyn. 230:403-409(2004)
                                                                                                                                                                                               Query Match
Best Local Similarity 77.0.
77 Conservative
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86 TRLRRODVGLK 96
                                                                                                                                                                                                                                                                                                                                                           2 RLTRKDRGL 10
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19 OLSRKDRGL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

XRAIN=56601 / Jarag X.-G., Zeng R., Miao Y.-G., Xu H.,

Ren S.-X., Fu G., Jarag R., Miao Y.-G., Xu H.,

Ren S.-X., Fu G., Jarag R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Xhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Xa J.-G., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Xa J.-G., Zhao G.-F., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.; Whole-genome sequencing.";

Interrogans revealed by whole-genome sequencing.";

Nature 422:888-893(2003).

Ren Shell, AROINISIS, ARAN88691;

Roj GO:0003905; F:alkylbase DNA N-glycosylase activity; IEA.

GO; GO:000578; F:alkylbase DNA N-glycosylase activity; Donds; IEA.

GO; GO:000578; P:ase-excision repair; IEA.

InterPro; IPR011257; DNA-glycsylse.

InterPro; IPR011257; DNA-glycsylse.

InterPro; IPR011255; Bnd-Jac.
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Naschento A.L.T.O., Ko.A.I., Martins E.A.L., Monteiro-Vitorello C.B., Naschento A.L.T.O., Ko.A.I., Martins E.A.L., Monteiro-Vitorello C.B., Marques M.D., Verjovski-Almeida S., Hartskeerl R.A., Carrer H., Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H., Perro B.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglaioti E.A., Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T., Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
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                                                                                                                                                                                                                             Name=magl; OrderedLocusNames=LA1370;
Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, Glycosidase, Hydrolase.
SEQUENCE 213 AA; 24567 MW; 01C4CA3DB9259732 CRC64;
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24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DNA-3-methyladenine glycosylase (EC 3.2.2.21).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 AA.
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                                                                                                         Created)
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ALKA OR LIC12362.
                                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00478; ENDO3c; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
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                                              PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=Fiocruz L1-130;
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QLSRKDRGL
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Search completed: January 13, 2005, 01:51:10 Job time : 87.8361 secs
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05-JUL-2004 (Rel. 44, Last annotation update)
Urease gamma subunit (EC 35.1.5) (Urea amidohydrolase gamma subunit).
Name=ureA; OrderedLocusNames=Cg10084, cg0113;
Corymbbacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteriae; Corymebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                            Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Derzose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V., Zouine M., Glaser P., Boemer N., Danchin A., Kunst F., "The genome sequence of the entomopathogenic bacterium Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Elkmanns B.J., Gaigalat L., Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A., Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nolden L., Beckers G., Moeckel B., Nampoothiri M., Pfefferle W., Kraemer R., Burkovski A.;
"Urease of Corynebacterium glutamicum: sequence and organisation of corresponding genes and investigation of activity.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puskas L.G., Inui M., Yukawa H.; "Structure and transcriptional regulation of the urease operon of
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                                                                                                                                                                                                                                                                       67.3%; Score 37; DB 2; Length 960; 77.8%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                       1, Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          960 AA; 107431 MW; 1329711136B972B1 CRC64;
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                        Nat. Biotechnol. 21:1307-1313(2003).
EMBL; BX571862; CAE13380.1; -.
PhotoList; plu1085; -.
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                                              MEDLINE=22957627; PubMed=14528314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 43, Created)
                                                                                                                                                                                                                                                                                                        7; Conservative
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           Complete proteome. SEQUENCE 960 AA;
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                                                                                                                                                            luminescens."
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J. Biotechnol. 104:5-25(2003).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the urease gamma subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.5%; Score 36; DB 1; Length 100; 100.0%; Pred. No. 18; 0; Mismatches 0; Indels
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ProDom; PD002319; Urease gamma; 1.
TIGRPAMs; TIGR00193; urease gam; 1.
Complete proteome; Hydrolase.
SEQUENCE 100 AA; 11245 MW; A48F
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HAMAP; MF_00739; -; 1.
InterPro; IPR002026; Urease_gamma.
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Best Local Similarity 100.
Matches 7; Conservative
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